STIC-Biotech/Cl	nemLib	94181
From: Sent: To: Subject:	Jiang, Dong Thursday, May 15, 2003 6:49 PM STIC-Biotech/ChemLib 10/050,704	Priority: 4/9/99 HGS (Sopper, D.)
Please search	SEQ ID NO:125	(01/0)
-issued & Pub. -commercial		No utility Toby Pont Feethical Info. Specialist CM 6AOA 703-3584
Please send re Thank you ver		in 10D-08 (mail stop CM1-10D19).

Dong Jiang (78243)
703-305-1345
U.S. Patent and Trademark Office
Art Unit 1646
dong.jiang@uspto.gov
CM1-10D08
Mail stop: CM1-10D19

Da a alignment b/w SEQ 125 & 127.

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up: 5/16	Bibliographic:	DRLink:
Date Completed: / 5/1/9	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

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Sequence:
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Maximum DB seq length: 20
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1 AAB38349

AAB38349 standard; Protein; 627 AA.

31-JAN-2001 (first entry)

Human secreted protein encoded by gene 29 clone HOFND85.

Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.

Homo sapiens.

WO200061623-A1.

19-OCT-2000.

09-APR-1999; 26-APR-1999; 06-APR-2000; 2000WO-US08979 99US-0128693. 99US-0130991.

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Ni J, Komat Lafleur DW, Olsen HS, Young PE; Ni J, Komatsoulis GA, , Olsen HS, Ebner R, Rosen CA, Florence KA, Soppet DR, Moore PA; Shi Y; Birse CE;

WPI; 2000-647418/62

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95 MEARVERAVQKRQVLFLCVFLGMSWAGAEPLRYFVAEETERGTFLTNLAKDLGLGVGELR 154

1 MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS 60

Matches

Local

Similarity

86.2%;

Score 2766; DB 22; Pred. No. 4.2e-238; Mismatches

Length 889; Indels

4.2e-238; hes 57;

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CC The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC in cestore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as cC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CT in polypeptide and polynucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
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ABG23879
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                                                 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, use diagnostics, forensics, gene mapping, identification of m responsible for genetic disorders or other traits and to hindiversity
Sequence
                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 54238; 103pp; English
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23-AUG-2000;
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23-AUG-2000;
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                                                                       Drmanac RT, Liu C,
                                                                                                   (HYSE-) HYSEQ INC.
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New isolated polynucleotide and encoded polypeptides, useful
                           N-PSDB; AAS88063
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                                                                                                                                                                                                                                                                                        supplement;
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                                            2001-639362/73
                                                                                                                                                                                                                                                                                        chromosome mapping; gene mapping; gene therapy;
upplement; medical imaging; diagnostic; genetic 
                                                                                                                              2000US-0540217
2000US-0649167
                                                                         YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 54235; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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Matches Sequence Local . Similarity 834 AA; Conservative 80.7%; Score 2587.5; DB 22 74.9%; Pred. No. 3.6e-222; 75. Mismatches 61; DB 22; Indels 75; Gaps u ٠٠

ДЬ 밁 γQ 밁 δÃ Вр Ωy QΥ 20 Š В Š В Ş 밁 Ър 밁 301 301 241 241 181 181 121 121 421 421 361 361 481 13 61 1 MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN 300 LWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVVFHI 180 ARGTRIVSDQNMQILLLSSLTGDLLLNEKLDREELCGPREPCVLPFQLLLEKPFQIFRAE ARGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAE 120 MEARVERAVQKRQVLFLCVFLGMSWAGAEPLRYFVAEETERGTFLTNLAKDLGLGVGELR 60 NVHDSGEGNIYPELVLNQVLDREEIPEFSLTLTALDGGSPPRSGTALVRILVLDVNDNAP NVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVP LWVRDINDHASVFLDREISLKILESTTPGAAFLLESAQDSDVGTNSLSNYTISPNAYFHI ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT 420 ITYTDLGTPRLKTEHNITYLVSDVNDNAPAFTQTSYTLFVRENNSPALPIGSVSATDRDS PETVVAVFRIRDRDSGNNGKTVCSIQDDLPFILKPSVENFYTLVTEKPLDRERNTEYNIT GTNAQVIYSLLPSQDPHLPLASLVSINADNGHLFALSPWTTMPLRAFEFRNNSPALHIGS 480 360 240 484

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485

541 VSTAETNIQVTYSLLPPRNPHLPLASLVSINTDNGHLFALRSLDYEALQEFEFRVGASDR

-----QVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADR

Matches

493;

Conservative

37;

Pred. No. 3.9e-212; 7; Mismatches 58;

Indels

65;

Gaps

2

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Best Local Similarity 75.5%;

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                                       a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
Sequence
                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                   for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                          polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
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diagnostic; genetic disorder.
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Query Match

77.18;

Score 2473.5;

DB 22;

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                                                                                                                                 WO200175067-A2
                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                      medical imaging; diagnostic; genetic
                                                                                                                                                                                                     forensic;
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polymerase chain reaction (PCR) primers, oligoners, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligoners, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligoners, and for chromosome and gene mapping, and in recombinant production of (II). The polymerased sare also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human that a polymer is the printed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS81344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT 420
                                                                                                                                                                                                                                                                                                                       VNLRSPLDFEVIQSYTINIQATDGGGLSGKCTLLVKVMDINDNPPEVTISSITKRIFENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFPQSLYEVQVPEDRPLGSWIATISAKDLDAGNYGKISYTFFHASEDIRKTFEINFISGE 300
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                                                                              ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS
                                                                                                                                                             SETLVALFSILDQDSGDNGRMICSIQDNLPFFLKPTFKNFFTLVSEKALDRESQAEYNIT
                                                                                                                                                                                                                                                                                                                                                                                                  LHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SREARVVSDDNKKYLHLDLLTGNLLLLNEKLDRDELCGSTEPCVLHFQVVLENPLQFFRFE
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ITVTDLGTPRLKTEYNITVLLSDVNDNAPTFTQTSYTLFVR#NNSPALHIGSVSATDRDS
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71.3%;
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10 QKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEEI

Matches 447; Query Match Best Local Similarity

Conservative

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AAR86865
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                                                   proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These sequences were isolated using primers 1 and 2 (see ANT03575 and ANT03576) The proteins may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding a
                                                                                                                                                                                                                                                                                          AR86865-R86867 represent the sequences for three protocadherins. This sequence represents the human protocadherin pc3. These sequences are related to cadherin, and possess cell adhesive ability. Cadherins are glycosylated integral membrane proteins that are involved in cell-cell glycosylated integral membrane proteins that are involved in cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR86865 standard; Protein; 787 AA.
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                                                                                                                                                                                                              the cytoskeleton through catenins and other cytoskeleton associated
                                                                                                                                                                                                                                    which consists of 5 unique subdomains, a membrane spanning domain, and a C-terminal cytoplasmic domain. The cytoplasmic domain interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide(s) encoding human protocadherins pc3 pc5 - involved in cell-cell adhesion and regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT03572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocadherin; pc3;
                                      protocadherins, and
                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 115-119; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-068873/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-1995;
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                                                                                                                                                                                                                                                                           Cadherins are composed of an N-terminal extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0268161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pc4; pc5; human; rat; cadherin;
                                    can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                  and pc4 and rat
activities
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                                                                                                                                                                                                                        Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO1899; PRO1899; PRO1887; PRO4785; PRO4353; PRO4357; PRO4405; PRO4356; PRO4352; PRO4354; PRO4508; PRO5737; PRO4425; PRO5990; PRO6030; PRO4424; PRO4422; PRO4499; tumour; obesity; diabetes; insulinemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
                              Modified-site
                                                            Modified-site
                                                                                              Modified-site
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     A novel polypeptide designated PRO4352.
                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2001 (first entry)
                                                                                                                                                                                                                   Crohns disease.
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                          /note=
53..59
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27..33
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                                                                                                          "signal peptide"
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09-DEC-1999;
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Novel secreted and transmembrane polypeptides useful for tumour in a mammal, for identifying agonists and antagoni
                                                       N-PSDB; AAA96347.
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                                       TEPGLFGVWAHNGEVRTA 627
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Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals

in mammals

WPI; 2001-602746/68. N-PSDB; AAS46163.

KP, Chen J, , Smith V, 1

Watanabe Desnoyers L,

CK,

Wood WI,

Goddard A, Gc ood WI, Zhang

Godowski 2

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25-APR-2000;
25-APR-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU29262 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU29262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO polypeptide; mammal; tumour; cancer; human; cattle; horse;
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                                                                                                                                                                                                                                                                                                        04-APR-2000;
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22-AUG-2000;
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05-JUN-2000;
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17-MAY-2000;
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.8-APR-2000;
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2000WO-US15264.
2000US-209832P.
2000WO-US20710.
2000US-0644848.
2000WO-US23328.
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2000WO-US08439.
2000US-194449P.
2000US-194647P.
2000US-195975P.
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2000US-199397P.
2000US-199550P.
2000US-199654P.
2000US-201516P.
2000US-201516P.
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2000WO-US32678
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Best Local
610 TEPGLFGVWAHNGEVRTA 627
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                                                                                                   LVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA 609
                                                                        LVLDANDNSPFYLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKA
                                                                                                                                                                LLPPQDPHLPLASLVSINADNGHLFALRSLDYEALQAFEFRVGATDRGSPALSREALVRV
                                                                                                                                                                                           LLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRV
                                                                                                                                                                                                                                                                                    RLKTQHNLTYTYSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTYS
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                                                                                                                                                                                                                                                                                                                                                                 IRDRDSGNNAKMVCSIQDHLPFYLKPSVENFYTLVTERÅLDREERTEYNITITVTDLGTP 429
                                                                                                                                                                                                                                                                                                                                                                                                                              ELVNSYKINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSPETVVAVFR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGNLHLKAELNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNKQYLLLDSHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDINDH
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                                                                                                                                                                                                                                                      RLKTEHNITVLVSDVNDNAPAFTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM 189
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RESULT 9

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                                                                                                                                                            Matches 441;
                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 53573; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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DNEQGLQLDLQTGQLILNEKLDREKLCGPTEPCIMHFQVLLKKPLEVFRAELLVTDINDH 145
                                    ETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDH 129
                                                                             EQRQVLILLLLEVTLAGWEPRRYSVMEETERGSFVANLANDLGLGVGELAERGARVVSE 85
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DB; AAS87401.
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2000US-0649167.
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                                                                                                                                                                               71.1%;
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                                                                                                                                                                           Score 2237; DB 22;
Pred. No. 3.3e-190;
                                                                                                                                                        Mismatches 108;
                                                                                                                                                                                               DB 22;
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RESULT 10

AAY41746

ID AAY41746

AC AAY41

XX AY41

XX Human

XW Human

XW Human

XW Probe

KW Secre

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                                                                                                                                                                                                                                                                                                           Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
probe; blood coagulation disorder; cancer; cellular adhesion disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ41388, and AAX41685 to AAX41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 163; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular
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ALSSEALVRVVVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQN
                                ALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQN
                                                                                       SGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSP
                                                                                                                                     TITVTDLGTPMLITQLNMTVLIADVNDNAPAFTQTSYTLFVRENNSPALHIRSVSATDRD
                                                                                                                                                       TITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD 479
                                                                                                                                                                                                       APETVVALFSVSDLDSGENGKISCSIQEDLPFLLK-SAENFYTLLTERPLDRESRAEYNI
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                                                                 SGTNAQVTYSLLPPQDPHLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSP
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427; Conserv
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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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Goddard A,
Kljavin IJ,
Shelton DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO531 (UNQ332) protein sequence SEQ ID NO:405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB44302 standard; Protein; 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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DB; AAC78558.
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                                                                                                                                                                                                                                                                                                                                                                             O polypeptides and polynucleotides used in detection methods, t bloactive molecules to specific cells, and to modulate activities -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Filvaroff E,
Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuo SS, Na
Stewart TA,
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99US-0145698.
99US-0162506.
99WO-US28313.
99WO-US28551.
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99US-0123957.
99US-0126773.
99US-0130232.
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99WO-US31274.
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99WO-US30095.
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ľA, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Botstein D, Desnoyers L, Eaton DL; Fong S, Gao W, Gerber H, Gerritsen Grimaldi CJ, Gurney AL, Hillan KJ; ier MA, Pan J, Paoni NF, Roy MA; Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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RESULT 11
AAB24049
IID AAB2
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AC AAB8
XX
DT 25---
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Huma
KW Huma
KW Hum
KW Cytc
KW Immu
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                tumourigenesis; detection; neoplastic cell growth; proliferation;
cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
                                                                                                                                                             Human; tumour; diagnosis; neoplastic disease; identification; cancer;
                                                                                                                                                                                                Human PRO531 protein sequence
                                                                                                                                                                                                                                25-JAN-2001
                                                                                                                                                                                                                                                                                                AAB24049 standard; Protein; 798
                                                  WO200053754-A1
                                                                                                                immunological disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APETYVALFSVSDLDSGENGKISCSIQEDLPFLLK-SAENFYTLLTERPLDRESRAEYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIELKKQLDFEKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEFEQPFYRVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRRGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SARGCRIVSDETIGFLILNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA 119
                                                                                                                                                                                                                                                                                                                                                                                                 AWLSYQLLKATEPGLFGVWAHNGEVRTA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITVTDLGTPMLITQLNMTVLIADVNDNAPAFTQTSYTLFVRENNSPALHIRSVSATDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELQVIDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH 179
                                                                                                                                                                                                                                                                                                                                                                                  AWLSYQLLKATELGLFGVWAHNGEVRTA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYI.VAKVVAVDGDSGQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGTNAQVTYSLLPPQDPHLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLTRKRSDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNA
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                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2142; DB 21;
Pred. No. 2.5e-182;
6; Mismatches 133;
                                                                                                                                                                                                 SEQ ID
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                                                                                                                                                                                                 NO:18
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NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN

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PEFYESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG

PEFEQPFYRVQISEDSPYGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG

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CC inflammatory disorders and immunological disorders can be treated.

CC ARC58123 to ARC58224 represent hybridisation probes and PCR primers used in the isolation of the human PRO sequences. ARC58225 to ARC58241 and AR24041 to ARB24056 represent human PRO polynucleotide and protein
                                                                                                                                                                                                                                                                            Matches 427;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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12-MAR-1999;
29-MAR-1999;
29-APR-1999;
21-APR-1999;
28-APR-1999;
05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated antibody for use in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation mammals; including humans, and in monitoring tumor treatment -
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30-DEC-1999;
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02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                              sequences given in the exemplification of the present invention
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 181
                                  180
                                                                    121
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                                                                                                                                                                                                                            1 MEARVVHALQKRQVSLLCVFLGVSWAG-AEPLRYFVAEETERGTFLANLAIDLGLGVEEL
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 VLTRKRSDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNUNA
                 ELQVIDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFR
                                                                                     ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH 179
                                                                                                                                    SRRGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQA
                                                                                                                                                      SARGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA
                                                                                                                                                                                                        MEASGKLICROROVLESFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEOREF
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                                                                                                                                                                                                                                                                                                                                              798 AA;
                                                                                                                                                                                                                                                                          Conservative
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99WO-US31243
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99WO-US28313.
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                                                                                                                                                                                                                                                                                          66.8%;
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                                                                                                                                                                                                                                                                            66;
                                                                                                                                                                                                                                                                                            Score 2142; DB 21;
Pred. No. 2.5e-182;
                                                                                                                                                                                                                                                                          Mismatches 133;
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                                                                                                                                                                                                                                                                                                              DB 21;
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                                                                                                                                                                                                                                                                                                            Length 798;
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RESULT 13
AAB33433
ID AAB33.
XX AAB33433
AC AAB33
XX 29-JP
XXX Humar
XXX Humar
XX Humar
XX Humar
XX Haem
XW dern
XW haem
XW anti
XW ostc
XW aut
XW AB33

YE AB3

YE AB33

YE AB33

YE AB33

YE AB3

YE AB33

YE AB3

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04-MAY-1999;
14-MAY-1999;
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10-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune related disease; diagnosis; antiinflammatory; cardian; dermatological; antiarthritic; antitheumatic; immunosuppressive; haemostatic; antithyroid; antidabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
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Kabakoff RC,
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2000WO-US03565.
2000WO-US04341.
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Lu Y, Pan J,
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D, Shelton DL,
                                                                                                                                                                           Yan M;
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2000-572271/53. Henzel Ψ,

N-PSDB; AAC58598

Sixty four PRO polypeptides, useful in the diagnosis and treatment immune related disorders, e.g. systemic lupus erythematosis, rheuma arthritis, osteoarthritis, thyroiditis and diabetes mellitus rheumatoid of

Claim 33; Fig 40; 309pp; English.

anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33417 represent human PRO polynucleotide and protein sequences. proteins, anti-PRO antibodies, agonists and antagonists are useful treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, reumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO sequences given in the exemplification of the present invention. for

Sequence 798 AA;

QΥ Д Q B Qγ Matches 427; Query Match Best Local 120 ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH 179 61  $\vdash$ 1 MEARVVHALQKRQVSLLCVFLGVSWAG-AEPLRYFVAEETERGTFLANLAIDLGLGVEEL SRRGVRVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFQVLLESPFEFFQA SARGCRIVSDETIGFLILINPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA 119 MEASGKLICROROVLESFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEOREF 60 Similarity Conservative 66.8%; 66; Score 2142; Pred. No. 2. Mismatches DB 21; 2.5e-182; Indels Length 2; 120 59

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  2000US-220664P.
2000US-220666P.
2000US-220893P.
2000WO-US20710.
2000WO-US23522.
2000WO-US233522.
2000WO-US233528.
2000US-0000000P.
2000WO-US30873.
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2000US-220607P.
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Similarity

Length 798;

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The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polypucleotides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosing tumours, especially lung CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or Cliver tumour. The PRO polypeptides are useful for stimulating the CC proliferation of, or gene expression, in pericyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the release of tumour necrosis factor-alpha from human dermal CC fibroblast cells. The PRO polypeptide may also be used as molecular to ceptivations in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO CV protein sequences of the invention.
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01-DEC-2000;
20-DEC-2000;
20-DEC-2000;
20-DEC-2000;
28-FEB-2001;
10-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                      One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, re
                                                                                                                                                                                                                                                                                                                                      Claim 11; Figure 132; 359pp; English.
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Sequence
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DB; ABK33601.
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C, Gurney
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2000WO-US32678.
2000US-0747259.
2000WO-US34956.
2001WO-US06520.
2001US-0854280.
2001WO-US17092.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski PJ;
○ CK, Wood WI;
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Qy Ωy DЪ Qy DЬ γg Вb Qy DЪ Qy 망 Qy 밁 Query Match Best Local S Matches 427 360 301 300 241 240 181 180 121 120 61 60 1 MEARVVHALQKRQVSLLCVFLGVSWAG-AEPLRYFVAEETERGTFLANLAIDLGLGVEEL SARGCRIVSDETIGFLLLNPLTGDLLLNEXLDREELCGPTEPCVLPFQLLLEKPFQIFRA HEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREF APETVVALFSVSDLDSGENGKISCSIQEDLPFLLK-SAENFYTLLTERPLDRESRAEVNI SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI EIELKKQLDFEKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPEN PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG VLTRKRSDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNA ELQVIDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFR ELWYRDINDHSPYFLDREITLNILESTTPGATFLLESAHDSDYGINNLRNYTISSNYYFH PEFEQPFYRVQISEDSPYGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG Conservative 66.8%; Score 2142; DB 23; 68.0%; Pred. No. 2.5e-182; tive 66; Mismatches 133; 2 120 419 359 186 179 60 300 299 240 2

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RESULT 15
AAY94997
ID AAY9497
XX AAY94
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                 The invention relates to 40 human secreted proteins (AAY94981-y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following: cytokine activity; cell proliferation; differentiation; immune modulation; haematopoiesis regulation; tissue growth activity; haemostatic activity; haemostatic/chemokinetic activity; haemostatic and thrombolytic activity; anti-inflammatory activity; and tumour inhibition activity. The proteins may be administered to patients as
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24-AUG-1998;
09-SEP-1998;
                                                                                                                                                                                                                                                                                                                                       Claim 43; Page 291-293; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     New secreted or transmembrane proteins and polynucleotides encodinium. useful for treating neurodegenerative disorders, autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Valenzuela D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALPH-) ALPHAGENE INC.
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23-AUG-1999;
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23-DEC-1998;
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98US-0097659.
98US-0099618.
98US-0102092.
98US-01109978.
98US-0113645.
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99US-0379246
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regime. Diseases or conditions that may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns; ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzhelmer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. The present sequence represents one of the
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 WLSYQLLKATEPGLFGVWAHNGEVRTA 627
                                                                                                                               GANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPA
                                                          LSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNA
                                                                                                             GTNAQVNYSLLPSQDPHLPLASLVSINADNGHLFALRSLDYEALQGFQFRVGATDHGSPA
                                                                                                                                                                                                                                                                                                                                                           LHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENS
                                       LSSEALVRVLVLDANDNSPFVLYPLQNGSAPCTELVPWAAEPGYLVTKVVAVDGDSGQNA
                                                                                                                                                                                       ITVTDLGTPRLKTEHNITVLVSDVNDNAPAFTQTSYALFVRENNSPALHIGSISATDRDS
                                                                                                                                                                                                                                                                                     PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
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Pred. No. 3.4e-180;
7; Mismatches 122;
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Search completed: May 16, Job time: 44 secs

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Result
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Maximum Match 10
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3208
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Maximum Match 100%
Listing first 45 summaries
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US-08-253-702A-110
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US-08-453-695A-112
US-08-453-695A-112
US-08-453-702A-112
US-08-453-702A-107
US-08-453-274B-107
US-08-453-274B-107
US-08-453-702A-107
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US-08-453-695A-110
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                                                                                                     Query Match
Best Local Similarity
Matches 447; Conserv
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5708143and, Gr.
REGISTRATION NUMBER: 35,
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CORRESPONDENCE ADDRESS:
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TOPOLOGY:
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CITY: Chicago
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                                   10 EQRQVLILLLLEVTLAGWEPRRYSVMEETERGSFVANLANDLGLGVGELAERGARVVSE
                                                                    10 QKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
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 70 ETIGFLLLNPLTGDLLLNEKLDREEELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDH 129
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                                                                                                                     Score 2287; DB 1;
Pred. No. 2.4e-207;
                                                                                                       Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
                                                                                                                                                                                                                                                                                               STREET: 22.
STREET: 111inois
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                             TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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TELEPHONE: 312/474-0448
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                                                                                                                             APPLICATION NUMBER: US/08/
FILING DATE: June 27, 1994
CLASSIFICATION: 435
                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                      60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Protocadherin Materials and Methods
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                                                                27866/32149
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                                                                                                                                                                  Sequence 110, Application US/08453702A Patent No. 5891706 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                      APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11 MOLECULE TYPE:
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                           ADDRESSEE: Bor
STREET: 233 SO
CITY: Chicago
STATE: Illinoi:
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             COUNTRY:
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60606
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                                                         233 South Wacker, 6300 Sears Tower
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                                                                           Borun
                                                                                        Marshall, O'Toole, Gerstein, Murray,
                                                                                                                         Protocadherin Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.3%; Score 2287; DB 1; 72.3%; Pred. No. 2.4e-207;
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COMPUTER READABLE FORM:

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US-08-453-702A-110
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ATTORNEY/AGENT INFORMATION:
NAME: No. 5891706and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                      610 TEPGLFGVWAHNGEVRTA 627
                                                                                                                                                          550 LVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA 609
                                                                                                                                                                                                                   490 LLPPQDPHLPLTSLVSINTDNGHLFALQSLDYEALQAFEFRVGATDRGFPALSSEALVRV
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TOPOLOGY: linear
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TELEX: 25-3856
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                               LLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRV 549
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TEPGLFGVWAHNGEVRTA 627
                                                                                                         LVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                   IRDRDSGENGKMICSIQDDVPFKLKPSVENFYRLVTEGALDRETRAEYNITITIDLGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patent In Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/263,161
FILING DATE: 27 JUN 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 25-3856
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CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130
370 IRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGTP 429
                                                                          310
                                                                                                                                                                                                                      250 QVPENSPVGSLVVKVSARDLDTGTNGEISYSLYYSSQEIDKPFELSSLSGEIRLIKÄLDF
                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                           190 KYPELVLDTELDREEQAELRLTLTAVDGGSPPRSGTVQILILVLDANDNAPEFVQALYEV
                                                                                                                                                                                                                                                                                                                                                                                                                  190 VYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Greta E. NO. 6262237and REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                 EAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSPETVVAVFR 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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312/474-0448
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PCT-US95-08071-110
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                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 787 amino acids
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                       TELEPHONE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Protoca
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                                                                                       Local
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29 DEC 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 23 DEC 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 S
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                            NAME: Noland, Greta E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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EQRQVLILLLLEVTLAGWEPRRYSVMEETERGSFVANLANDLGLGVGELAERGARVVSE 69
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                                                                         al Similarity 447; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKA
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                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                      312/474-0448
                                                                       Conservative
                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version
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                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                     71.3%; Score 2287; DB 5; 72.3%; Pred. No. 2.4e-207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
             REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                ATTORNEY/AGENT INFORMATION: NAME: No. 5708143and, Gr
                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                    STREET: 250
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                REGISTRATION NUMBER:
                                                                                              CLASSIFICATION:
                                                                                                                   FILING DATE:
                                                                                                                                                                  SOFTWARE:
 TELEPHONE:
                                                                                                                                                                                                                                                                 COUNTRY:
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                                    INT INFO...
5708143and, Grec.
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312/474-6300
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                                                                                                                                 US/08/453,695A
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RESULT 7
US-08-268-161A-112
; Sequence 112, Application US/08268161A
; Patent No. 5798224
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
TYPE: amino acid
                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                             APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials
NUMBER OF SEQUENCES: 115
STREET: 22.
STREET: 111inois
                                                                                                                         CORRESPONDENCE ADDRESS:
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TELEX: 25-3856
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                                       ADDRESSEE: BOILING ADDRESSEE: 233 South Wacker,
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                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELQLTDINDHSPEFPNKKMLLTIPESAHPGTVFPLKAARDSDIGSNAVQNYTVNPNLHFH 179
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                                                                 Sears Tower
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-268-161A-112
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Best Local Similarity 62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
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TELEFAX: 25-3856
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TYPE: a
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TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Young J. Suh
REGISTRATION NUMBER: P-4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTED: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: June 27, 1994
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                                                                                                                    SGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSP 539
                                                                                                                                                                   TITVSDLGTPRLTTQHTITVQVSDINDNAPAFTQTSYTMFVHENNSPALHIGTISATISD
                                                                                                                                                                                                 TITYTDLGTPRLKTQHNLTYTYSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD 479
                                                                                                                                                                                                                                    SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI
                                                                                                                                                                                                                                                                                                     EIHLSKELDFEEISNHNIEIAATDGGGLSGKCTVAVQVLDVNDNAPELTIRKLTVLVPEN
                                                                                                                                                                                                                                                                                                                         NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDÎNDNPPELLMSSLTSPIPEN 359
                                                                                                                                                                                                                                                                                                                                                                      PQFVQSLYKVQVPENNPLNAFVVTVSATDLDAGVYGNVTYSLFQG-YGVFQPFVIDE1TG
                                                                                                                                                                                                                                                                                                                                                                                        PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
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AWLSYQLLKATEPGLFGVWAHNGEVRT
                                 ALSSQTLVRMVVLDDNDNAPFVLYPLQNASAPCTELLPRAAEPGYLITKVVAVDRDSGQN
                                                                                                  SGSNAHITYSLLPPDDPQLALDSLISINVDNGQLFALRALDYEALQSFEFYVGATDGGSP
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILLY CLASSIFICATION: ****
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5891706and, Greta
NAME: NO. 5891706and, Greta
NAME: NO. 5891706and, Greta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
360 SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI 419
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CTTY: Chicago
                                              299 EIHLSKELDFEEISNHNIEIAATDGGGLSGKCTVAVQVLDVNDNAPELTIRKLTVLVPEN
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                                                                                                                                                                                                                                                          180 INVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNV 239
                                                                                                                                                                                                                                                                                                                                         120 ELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEARVVHALQKRQVSLLCVFLGVSW-AGAEPLRYFVAEETERGTFLANLAIDLGLGVEEL
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                                                                                     NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN 359
                                                                                                                                                                                                                                                                                                   ELQLTDINDHSPEFPNKKMLLTIPESAHPGTVFPLKAARDSDIGSNAVQNYTVNPNLHFH
                                                                                                                             PQFVQSLYKVQVPENNPLNAFVVTVSATDLDAGVYGNVTYSLFQG-YGVFQPFVIDEITG
                                                                                                                                                                      PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.6%; Score 2009.5; DB 2; Length 797; 62.7%; Pred. No. 4.5e-181; 4; ative 83; Mismatches 148; Indels 3;
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60 SARGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA 119

1 METALAKIPQQRQVFFLTI-LSLLWKSSSEAIRYSMPEETESGYMVANLAKDLGIRVGEL 59

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US-09-099-639-112
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                                  Matches
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                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                      SEQUENCE CHARACTERISTICS: LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Greta E. No. 6262237and
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patent In Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CTTY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suzuki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479
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                                                                                                                                                                                                       TELEPHONE: 312, 100448
                                               Local Similarity
                                                                                                                         TOPOLOGY:
                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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1 MEARVVHALQKRQVSLLCVFLGVSW-AGAEPLRYFVAEETERGTFLANLAIDLGLGVEEL 59
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                                Conservative
                                                                                                                            linear
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                              27 JUN 1994
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                                            62.6%; Score 2009.5; DB 4 62.7%; Pred. No. 4.5e-181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protocadherin Materials and Methods
                                                                                                                                                                                                                                                                                                                                             US 08/263,16
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                                                                                                                                                                                                                                                                             35,302
                               83;
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                               Mismatches
                               148;
                                                            DB 4; Length 797;
                               Indels
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                             Gaps
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PCT-US95-08071-112; Sequence 112, Application PC/TUS9508071; GENERAL INFORMATION:
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12588
FILING DATE: 23 DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,003
APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: NOISON GREAT F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials
NUMBER OF SEQUENCES: 115
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 32149
                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                     PCT/US95/08071
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RESULT 11
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
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TELEFAX: 25-3856
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es 393; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEARVVHALQKRQVSLLCVFLGVSW-AGAEPLRYFVAEETERGTFLANLAIDLGLGVEEL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SARGCRIVSDETIGELLLNELTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRA 119
                                                                                                                                                                                                                                                                           TITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD
                                                                                                                                                                                                                                                                                                                                                                                             EIHLSKELDFEEISNHNIEIAATDGGGLSGKCTVAVQVLDVNDNAPELTIRKLTVLVPEN
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                                                                                                                                                                                                                                                                                                                             SAETVVAVESVSDSDSGDNGRMYCSIPNNIPFLLKPTFENYYTLVTEGPLDRENRAEYNI
                                                                                                                                                                                                                                                                                                                                                             SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQFVQSLYKVQVPENNPLNAFVVTVSATDLDAGVYGNVTYSLFQG-YGVFQPFVIDEITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
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                                                                                                                                       ALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQN
                                                                                                                                                                                                                                                                                                                                                                                                                               NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN
                                                AWLSFQLLKATEPGLFSVWAHNGEVRT
                                                                                 AWLSYQLLKATEPGLFGVWAHNGEVRT
                                                                                                                  ALSSQTLVRMVVLDDNDNAPFVLYPLQNASAPCTELLPRAAEPGYLITKVVAVDRDSGQN
                                                                                                                                                                                     SGSNAHITYSLLPPDDPQLALDSLISINVDNGQLFALRALDYEALQSFEFYVGATDGGSP
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62.7%;
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US-07-998-003A-107; Sequence 107, Application US/07998003A; Patent No. 5643781; GENERAL INFORMATION:

APPLICANT:

Suzuki, Shintaro

Protocadherin Materials 107

and

Gerstein, Murray,

CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NUMBER OF SEQUENCES:

ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Bicknell STREET: 20 South Clark Street

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В
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
554 IFVTDRNDNAPQVLYPRPGGSS--VEMLPRGTSAGHLVSRVVGWDADAGHNAWLSYSLFG 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                       549 VLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLK 608
                                                                                                             494 FLLEQGAETGLVGRYFTINRDNGIVSSLVPLDYEDRREFELTAHISDGGTPVLATNISVN 553
                                                                                                                                                            489 SLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVR 548
                                                                                                                                                                                                                                                                      429 PRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTY 488
                                                                                                                                                                                                                                                                                                                           374 SVTDLDAGENGLVTCEVPPGLPFSLTSSLKNYFTLKTSADLDRETVPEYNLSITARDAGT
                                                                                                                                                                                                                       434 PSLSALTIVRVQVSDINDNPPQSSQSSYDVYIEENNLPGAPILNLSVWDPDAPQNARLSF
                                                                                                                                                                                                                                                                                                                                                                                 369 RIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                      314 DTKLHEIYIQAKDKGANPEGAHCKVLVEVVDVNDNAPEITVTSVYSPVPEDASGTVIALL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AIQTYTLTIQAKDGGG--LSGKCTVVVHYTDINDNPPELLMSSLTSPIPENSPETVVAVF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 PENSPVGSLVVTVSARDLDTGSNGEIVYAF-FYATERTLKTFRINSTSGNLHLKAELNYE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 AELVLERALDREREPSLQLVLTALDGGTPALSASLPIHIKVLDANDNAPVFNQSLYRARV 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 SELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 AFPTQEMKLEISEAVAPGTRFPLESAHDPDLGSNSLQTYELSRNEYFALRVQTREDSTKY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 VELDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGNVY 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: NO. 5643781and, Greta
REGISTRATION NUMBER: 35,302
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGGCTSGTRVVQVLATDLDEGPNGEIIYSFGSHNRAGVRQLFALDLVTGMLTIKGRLDFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVVGVL-LLLGALNKASTVIHYEIPEEREKGFAVGNVVANLGLDLGSLSARRFPVVSGAS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSP 131
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US-08-453-274B-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFFILING DATE: 30-MAY-177,
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5663300and, Greta
NAME: NO. 5663300and, Greta
NAME: NO. 1563300and, Greta
NAME: NO. 35,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 682 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
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    369
                                                                                                                                                                                                                                   192 SELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQV 251
                                                                                                                                                                                                                                                                                                                     132 VFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGNVY 191
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                                                                                 311 AIQTYTLTIQAKDGGG--LSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSPETVVAVF 368
                                                                                                                                                                   252 PENSPYGSLYVTYSARDLDTGSNGEIYYAF-FYATERTLKTFRINSTSGNLHLKAELNYE 310
                                                                                                                                                                                                             194 AELVLERALDREREPSLQLVLTALDGGTPALSASLPIHIKVLDANDNAPVFNQSLYRARV 253
                                                                                                                                                                                                                                                                                               134 AFPTQEMKLEISEAVAPGTRFPLESAHDPDLGSNSLQTYELSRNEYFALRVQTREDSTKY 193
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TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                 74 RREFEVNRETGEMEVNDRLDREELCGTLPSCTVTLELVVENPLELFSVEVVIQDINDNNP
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TELEFAX: 312/474-0448
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RIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGT 428
                                       DTKLHEIYIQAKDKGANPEGAHCKVLVEVVDVNDNAPEITVTSVYSPVPEDASGTVIALL 373
                                                                                                                             PGGCTSGTRVVQVLATDLDEGPNGEIIYSFGSHNRAGVRQLFALDLVTGMLTIKGRLDFE 313
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60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.9%; Score 1217; DB 1; llarity 41.0%; Pred. No. 3.3e-106; Conservative 117; Mismatches 242;
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South Wacker
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US-08-453-695A-107
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                                                                                                                                    Matches
                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: No. 5708143and, Greta REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                      Local Similarity
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                                                                                             RQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSDET 71
RRFFEVNRETGEMFVNDRLDREELCGTLPSCTVTLELVVENPLELFSVEVVIQDINDNNP 133
                              IGFLILINPLTGDLLLINEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSP 131
                                                                   RVVGVL-LLLGALNKASTVIHYEIPEEREKGFAVGNVVANLGLDLGSLSARRFPVVSGAS 73
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                                                                                                                                    Conservative
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41.0%;
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                                                                                                                                    117;
                                                                                                                                                                                                                                                                                                         107:
                                                                                                                                  Score 1217; DB 1;
Pred. No. 3.3e-106,
7; Mismatches 242.
                                                                                                                                                                                                                                                                                                                                                                                            32658
                                                                                                                                                      3.3e-106;
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US-08-268-161A-107
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                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                SEQUENCE CHARACTERISTICS:
                                                                                                REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Young J. Suh
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                                         TELEFAX: JI.,
TELEFAX: 25-3856
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                          REGISTRATION NUMBER: P-41,337
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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682 amino acids
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RESULT 15
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; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-268-161A-107
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                                                                                                                                                                                                                                                             Sequence 107, Application US/08453702A Patent No. 5891706 GENERAL INFORMATION:
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                             STREET: 233 SO
CITY: Chicago
STATE: Illinoi
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     COMPUTER:
                                                                          COUNTRY:
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                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
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                                                             60606
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                                                                                                                          233 South Wacker, 6300 Sears Tower
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IBM PC compatible
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41.0%; Pred. No. 3.3e-106;
ative 117; Mismatches 242;
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NO. 5891706and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 326
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                             494
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APPLICATION NUMBER: US/08/453,702A
                                                                554 IFVTDRNDNAPQVLYPRPGGSS--VEMLPRGTSAGHLVSRVVGWDADAGHNAWLSYSLFG
                                                                                                                                                                              489
                                                                                                                                                                                                        434 PSLSALTIVRVQVSDINDNPPQSSQSSYDVYIEENNLPGAPILNLSVWDPDAPQNARLSF
                                                                                                                                                                                                                                                                          374 SYTDLDAGENGLYTCEVPPGLPFSLTSSLKNYFTLKTSADLDRETVPEYNLSITARDAGT
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  429
                                                                                                                                                                                                                                                                                                                                                                                311 AIQTYTLTIQAKDGGG--LSGKCTVVVHVTDINDNPPELLMSSLTSPIPENSPETVVAVF
                                                                                                                                                                                                                                                                                                                                                                                                                            254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 VFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGNVY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 IGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 RVVGVL-LLLGALNKASTVIHYEIPEEREKGFAVGNVVANLGLDLGSLSARRFPVVSGAS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 RQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSDET 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                           ATEPGLEGVWAHNGEVRTA 627
                                                                                               VLVADANDNAPFVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLK 608
SPNQSLFAIGLHTGQISTA
                                                                                                                                     FLLEQGAETGLVGRYFTINRDNGIVSSLVPLDYEDRREFELTAHISDGGTPVLATNISVN
                                                                                                                                                                   SLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVR 548
                                                                                                                                                                                                                                          PRIKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTY
                                                                                                                                                                                                                                                                                                                                                 DTKLHEIYIQAKDKGANPEGAHCKVLVEVVDVNDNAPEITVTSVYSPVPEDASGTVIALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEEVESLYKVQV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRFFEVNRETGEMFVNDRLDREELCGTLPSCTVTLELVVENPLELFSVEVVIQDINDNNP 133
                                                                                                                                                                                                                                                                                                                                                                                                                     PGGCTSGTRVVQVLATDLDEGPNGEIIYSFGSHNRAGVRQLFALDLVTGMLTIKGRLDFE 313
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PatentIn Release #1.0, Version #1.25
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41.0%; Pred. No. 3.3e-106;
tive 117; Mismatches 242;
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Search completed: May 16, 2003, 10:49:15 Job time: 20 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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PIR_73:*
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N-cadherin precurs	150116	2	783	11.0	351.5	45
cadherin 3 precurs	IJHUCP	۳	829	11.0	353	44
E-cadherin precurs	IJCHCL	ш	887	11.1	354.5	43
hypothetical prote	T34563	N	373	11.2	360.5	42
cadherin 5 precurs	ілнис5	ᆫ	784	11.3	361.5	41
N-cadherin precurs	IJCHCN	Ц	912	11.7	374	40
cadherin 11 precur	A38992	N	796	11.8	378	39
cadherin - African	S47518	N	871	11.9	380.5	38
OB-cadherin precur	A53584	Ν	796	11.9	380.5	37
cadherin 2 precurs	IJHUCN	-	906	11.9	382	36
cadherin-11 - mous	I49556	N	796	11.9	382	ω 5
hypothetical prote	T46413	N	709	11.9	383	34
cadherin-11 - mous	148277	N	796	12.0	384.5	$\frac{\omega}{\omega}$
N-cadherin precurs	IJMSCN	۲	906	12.0	386.5	32
N-cadherin precurs	IJBOCN	ب	877	12.2	390	31
G-cadherin - sea u	T30213	N	2809	12.3	395	30

## ALIGNMENTS

R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, September 1999 A;Reference number: Z18722 A;Accession: T17243

A; Experimental source: adult uterus; clone DKFZp586B0217 C; Genetics:

A; Note:

DKFZp586B0217.1

A; Molecule type: mRNA A; Residues: 1-701 <KOE>

A; Status: preliminary

A; Cross-references: EMBL: AL117449

C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999
C;Accession: T17243

human (fragment)

hypothetical protein DKFZp586B0217.1 -

precu prote ΩV В Qγ 밁 Ωy 밁 Qy Вþ Qy Ъ 20 밁 QY В 20 Query Match Best Local : Matches 381; 121 515 300 395 181 155 ESAHDSDYGINNLRNYTISSNYYFHINYHDNGEGNYYSELYLDKYLDREEYPELRLTLTG 360 275 95 LCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSPVFLDREITLNILESTTPGATFLL 154 61 KIAODFDIGSNTVONYTISPNSHFHVATHNRGDGRKYPELVLDKALDREERPELSLTLTA MCGATEPCILHFQLLLENPVQFFQTDLQLTDINDHAPEFPEKEMLLKIPESTQPGTVFPL TYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLF PSVENFYTLVTERALDREERTEYNITITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQT GSVAYALFQGDEVT-QPFVIDEKTAEIRLKRALDFEATPYYNVEIVATDGGGLSGKCTVA GEIVYĄFFYATERTLKTFRINSTSGNLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVV ALRSIDFEALQAFEFRYGAADRGSPALSSQALVRVLVADANDNAPFVLYPLQNGSAPCTE LDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSN SYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQNPHLRLASLVSINADNGHLF LDGGAPPRSGTTTIRIVVLDNNDNAPEFLQSFYEVQVPENSPLNSLVVVVSARDLDAGAY 180 PTLKNFYTLVTQRTLDRESQAEYNITITVTDMGTPRLKTEHNITVLVSDVNDNAPAFTQT Similarity Conservative 62.0%; 71.5%; 58; Score 1989.5; DB Pred. No. 3e-124; Mismatches DB 2; 93; Indels Length 701; 1. Gaps 454 239 574 359 299 394 274 214 60 1:

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submitted to the EMBL Data
A;Reference number: Z16540
A;Accession: T09055
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C; Species: Homo sar
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;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
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-ELQVPRNAGLGYLVSTVRALDSDFGESGRLTYEIVDGNDDHLFEIDPSSGEIRT
                                                                                              ALRSLDFEALQAFEFRVGAADRGSPA-LSSQALVRVLVADANDNAPFVLYP-LQNGSAPC
                                                                                                                                                LYVLQVHENNIPGDXLGSVLAQDPDLGQNGTVSYSILPSHIGDVSIYTYVSVNPTNGAIY
                                                                                                                                                                                                                    SSLTSPIPENSPETVVAVFRIRDRDSGNNAKMVCSI------QDHLPFVLK
                                    TEL-VPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAHNGEVRT 626
                                                                        ALRSFNFEQTKAFEFKVLAKDSGAPAHLESNATVRVTVLDVNDNAPVIVLPTLQNDTA--
                                                                                                                                                                                                                                                                                              GALSEAAP----PGTVIALVRVTDRDSGKNGQLQCRVLGGGGGTGGGGGGLGGPGGSVPFKLE
                                                                                                                                                                                                                                                                                                                                                                                                        TSGNLHLKAELNYEAIQTYTLTIQAKDGGG--LSGKCTVVVHVTDINDNPPEL----LM
                                                                                                                                                                                    {\tt TYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLF}
                                                                                                                                                                                                                                                                                                                                                                    KTGLIRVKGNLDYEENGMLEIDVQARDLGPNLIPAHCKVTVKLIDRNDNAPSIGFVSVRQ
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Pred. No. 1
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B

BH-protocadherin PCDH7 (clone BH-Pcdh-b) - human C:Species: Homo sapiens (man) C:Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 01-Dec-2000

R; Yoshida, K.

T00041;

T00040

Seki,

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Sasaki,

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Sugano,

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A;Residues: 1-1180 <TEL>
A;Cross-references: EMBL:Y08715; NID:g2764993; PIDN:CAA69965.1; PID:g2764994
A;Experimental source: brain capillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Identification of a novel cadherin (vascular endothelial A;Reference number: Z20962; MUID:98316322; PMID:9651350 A;Accession: T31066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vascular cadherin-2 - mouse
c;Species: Mus musculus (house mouse)
C;Date: 22-Oct.1999 #sequence_revision 22-Oct-1999 #text_change
C;Accession: T31066
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J. Biol. Ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 VKFQVTEEVPSGTVIGKLS-----QELRVEERRGKAGDAFQILQLPQALPVQMNSEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 LRYFVAEETERGTFLANLAIDLGLGVEELSARGCRIVSDETIGFLLL------NPLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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TIVARDADSGANGELFYSIQSGNDAHLF
                                      KVVAVDGDSGQNAWLSYQLLKATEPGLF
                                                                                                                       DNAPFVLYP-LQNGSAPCTELV---
                                                                                                                                                                                                                                                                    NLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDSGANAQVTYSLLPPHD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLTATDPDQGPNGEVEFFFGKHVSPEVMNTFGIDAKTGQIILRQALDYEKNPAYEVDVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVSARDLDTGSNGETVYAF-FYATERTLKTFRINSTSGNLHLKAELNYEAIQTYTLTIQA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SESASLHTRIPLDRALDQDTGPNSLYSYSLSPSEHFALDVIVGPDETKHAELVVVKELDR
                                                                              DNAPEVIQPVLSEGKATLSVLVNASTGHLLLPIENPSGMDPAGTGIPPKATHSPWSFLLL
                                                                                                                                                           KDSPVSHLVIIDFETGEVTAQRSLDYEQMAGFEFQVIAEDRGQPQLASSISVWVSLLDAN
                                                                                                                                                                                       PQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRVLVADAN
                                                                                                                                                                                                                                               ELQIQVSDVNDNAPVFEKSRYEVSTWENNPPSLHLITLKAHDADLGSNGKVSYRI-----
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                                                                                                                                                                                                                                                                                                                                                                  NNAKMYCSIQDHL-PFYLKPSYENFYTLYTERALDREERTEYNITITYTDLGTPRLKTQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDGG--GLSGKCTVVVHVTDINDNPPELLM--SSLTSPIPENSP-ETVVAVFRIRDRDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLSTSSRLDREKLCRQEDPCLVSFDVLATGASALIHVEIQVLDINDHQPQFPKDEQELEI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELHSYFDLVLTAYDNGNPPKSGISVVKVNVLDSNDNSPVFAESSLALEIPEDTVPGTLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKVQVPENSPVGSLVV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breviario, F.; Huber, P.; Panzeri, C.; Dejana, em. 273, 17565-17572, 1998
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1058,'M',1060,'LH',1063,'Y',1065,'TVFG' <Y02>
A;Cross-references: EMBL:AB006755; NID:g2979417; PIDN:BAA25194.1; PID:g2979418
A;Experimental source: clone BH-Pcdh-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 49, 458-461, 1998
A;Title: Cloning, expression analysis, and chromosomal localization of BH-protocadherin A;Reference number: 214074; MUID:98277460; PMID:9815233
A;Accession: 700041
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Belding: 1-1072 2000
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A;Cross·references: EMBL:AB006756; NID:g2979419; PIDN:BAA25195.1; PID:g2979420
A;Experimental source: clone BH-Pcdh-b
A;Accession: T00040
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--- VGMVTVMDADKGRNAEMS
                                              GYLVAKVVAVDGDSGQNAWLS
                                                                                                                                    FRVGAADRGSPALSSQALVRVLVADANDNAP-----FVLYPLQNGSAPCTELVPRAAEA
                                                                                                                                                                                                RVATVLATDADSGKNAEIAYSL-----DSSVMGIFAIDPDSGDILVNTVLDREQTDRYE
                                                                                                                                                                                                                             LNYEAIQTYTLTIQAKDGG--GLSGKCTVVVHVTDINDNPPEL-----LMSSLTSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGNLHLKAE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGEKQPQLIVKGALDREQRDSYELTLRVRDGGDPPRSSQAILRVLITUVNDNSPRFEKSV 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLDINDNTPTFPSPVLTLTVEENRPVGTLYLLPTATDRDFGRNGIERYELLQEPGGGGSG 192
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                                                                                                FKVNAKDKGIPVLQGSTTVIVQVADKNDNDPKFMQDVFTFYVKEN-----LQPNSP--
                                                                                                                                                                                                                                                                                                                                LDREERTEYNITITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPAL
                                                                                                                                                                                                                                                                                                                                                                                                 AEDVLVDTPIALVQVSDRDQGENGVVTCTVVGDVPFQLKPASDTEGDQNKKKYFLHTSTP 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                IPENSPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVE----NEYTLVTERA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEADLAENSAPGTPILQLRAADLDVGVNGQIEYVFGAATESVRRLLRLDETSGWLSVLHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYLKIDNLTGELSTSERRIDREKLPQCQMIFDENECFLDFEVSVIGPSQSWVDLFEGQVI 132
                                                                                                                                                                                                                                                                                                 LDYEATREFNVVIVAVDSGSPSLSSKNSLIVKVGDTNDNPPMFGQSVVEVYFPENNIPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDREEVNQLRFTVMARDRGQPPKTDKATVVLNIKDENDNVPSIEIRKIGRIPLKDGVANV 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 110; Mismatches 246; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.2%; Score 807; DB 2 30.4%; Pred. No. 2e-45;
                                                 603
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RESULT T00043

BH-protocadherin PCDH7 (clone BH-Pcdh-c) - human C;Species: Homo sapiens (man)

T00042

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... A; Map position:
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C; Species: Mus musculus (h
C; Date: 22-Jan-1999 #seque
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R; Yoshida, K.
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A; Residues: 1-1069 < YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AB006758;
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                                                                                                                                          531 VGAADRGSPALSSQALVRVLVADANDNAP-----FVLYPLQNGSAPCTELVPRAAEAGY 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 REEVNQLRFTVMARDRGQPPKTDKATVVFNIKDENDNVPSIEIRKIGRIPLKDGVANVAE 434
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les 209; Conserv
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                                           LVAKVVAVDGDSGQNAWLS 603
                                                                                              VNAKDKGIPVLQGSTTVIVQVADKNDNDPKFMQDVFTFYVKEN-----LQPNSP----
                                                                                                                                                                                                                                         GSVSATDRDSGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFR
                                                                                                                                                                                                                                                                                                                                        REERTEYNITITYTDLGTPRLKTQHNLTYTYSDVNDNAPTFSQTTYTLRVRENNSPALHI 470
                                                                                                                                                                                                                                                                                                                                                                                             DVLVDTPIALVQVSDRDQGENGVVTCTVVGDVPFQLKPASDTEGDQNKKKYFLHTSAPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                      ENSPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVE-----NFYTLVTERALD
-VGMVTVMDADKGRNAEMS
                                                                                                                                                                                             ATVLATDADSGKNAEIAYSL - - - -
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675
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                                                                                                                                                                                             -DSSV-MGTF-AIDPDSGDILVNTVLDREQTDRYEFK
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R;Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goodman, Cell 67, 853-868, 1991
                                                                                       cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster) (;Species: Drosophila melanogaster C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
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A;Residues: 1-1200 <YOS>
A;Cross-references: EMBL:AB006757; NID:g2979421; PIDN:BAA25196.1; PID:g2979422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 49, 458-461, 1998
A; Title: Cloning, expression analysis, and chromosomal localization of BH-protocadherin A; Reference number: Z14074; MUID:98277460; PMID:9615233
A; Accession: T00042
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C;Accession: T00042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 IRILVLDINDNVPE----FVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 HDNGEGNVYSELVLDKVLDREEVP------ELRLTLTGLDGGSPPRSGTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 VLDINDNTPTFPSPVLTLTVEENRPVGTLYLLPTATDRDFGRNGIERYEL------L
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193; Conser
                                                                       A41087; B41087
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tumor suppressor gene in Drosophila encodes a novel member of the cadhe
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: cadherin-related tumor suppressor; cadherin repeat homology: EGF C;Keywords: calcium binding; cell adhesion; duplication; transmembrane protein F;1-55/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1492-1601/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;718-822/Domain: cadherin repeat homology <CR7>F;831-942/Domain: cadherin repeat homology <CR8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;36-4583/Domain; extracellular #status predicted <EXT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1925-2027/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: FlyBase: FBgn0001075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: tat
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A;Note: 1229-Gly and 1233-Ser were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-142; 487-1278 <MA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 143-485; 1279-5147
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                                                                                                                                                                                             Matches
                                                                                                                                                                                                           Query Match
Best Local
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150 ATFILESAHDSDVGINNLRNY--TISSNV--YFHINVHDNGEGNV-YSELVLDKVLDREE
                                                       118
                                                                                     90
                                                                                                                    64 AVDTSADFEVLEGQPRG-----TTVGFIPTKPKFSYRFNEPPREFTLDPVTGEVKTNVV 117
                                                                                                                                                     49 AIDLGLGVEELSA--RGCRIVSDETIGFL----
                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167/Domain:
                                                   LDREGMRDHYDLVVLSSQ-----PTYPIEVRIKVLDVNDNSPEFPEPSIAISFSESATSG
                                                                                  LDREELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSPVFLDREITLNILESTTPG
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<C25>
<C26>
<C27>
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.3e-30;
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                                                                                                                                                                                                                                                           <TNI>
                                                                                                                                                                                                                       Length 5147;
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                                                                                                                                                       --- LLNPLTGDLLLNEK
                                                                                                                                                                                         Indels 172;
                                                                                                                                                                                      Gaps
                                                   172
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A; Map position: C; Keywords: trans
F; 1-26/Domain: s:
F; 27-3034/Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seven-pass transmembrane receptor protein precursor - mouse C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T14119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
T14119
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                                                                                                                                                                                                                                                                                                                                                                                                     R;Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R. submitted to the EMBL Data Library, October 1997
A;Description: The Celsr family of novel evolutionarily conserved
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                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AF031572;
                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-3034 <HAD>
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                                                                                                                                                           27-3034/Product:
                                                                                                                                                                                                   Keywords: transmembrane protein
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                                                                                                                                                           26/Domain: signal sequence #status predicted <SIG>
-3034/Product: seven-pass transmembrane receptor p
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                                                                                                Local Similarity
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  IVSGNLKGQFYLHSLSGSLDVINPLDFEAIREYTLRIKAQDGGRPFLINSSGLV-----
                           ----FVLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKATEPGLF
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                                                                                                18.2%;
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                                                                           Score 584; DB 2;
Pred. No. 6.4e-30;
5; Mismatches 245;
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                                                                                                                                                                                                                                                                                 NID:g3800735; PID:g3:00736;
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                                                                                                                   Length 3034;
                                                                                                                                                             protein #status
                                                                               indels
                                                                                                                                                                                                                                                                                     PIDN:AAC68836.1
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                                                                                                                                                             predicted <MAT>
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ASDSYNVTILENITIPAVIATVKATDEDFGTNGKVHYSMASSSGIGGLTIDYSTGEVTLR 435

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A; Delcube type: DNA
A; Molecule type: DNA
A; Residues: 1-2610 <WI2>
A; Cross-references: EMBL: Z78018; PIDN: CAB01449.1; GSPDB: GN00023; CESP: F1589.7
A; Cross-references: Cione W07G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F1589.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T20968; T26278
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                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, August 1996 A; Reference number: Z20187 A; Accession: T26278
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-2610 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A; Reference number: Z19351
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                                                                                                                         A; Introns: 169/2; 217/3; 239/3; 284/3; 515/2; 550/3; 738/3; 810/1;
                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                            R;Baynes,
                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone F15B9
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z78013; PIDN:CAB01427.1; GSPDB:GN00023; CESP:F1589.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T20968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Percy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T20968
                                                                                                                                                                  A; Gene: CESP:F15B9.7
                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
                                       Best Local Sir
Matches 172;
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36 AEETERGTFLANLAIDLGLGV-----EELSARG----CRIVSDETIGFLLLNPLTGDLLLN 87
                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKPSVENFYTLVTERALDREERTEYNITITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHVTDINDNPPELLMSSLTSPIPENSP-ETVVAVFRIRDRDSGNNAKMVCSIQDHLP-FV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFRAELWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDFYQGSVFEDAPPSTSVLQVSATDRDSGPNGRLLYTFQGGDDGD---GDFY-IEPTSGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASTIVGGSSVDSENPASAPDFPFQIHNSSGWITVCAE-----LDREEVEHYSFGVEAVD
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                                         Conservative 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPVGSVVARIRANDPDEGPNAQIIYQIVEGNVPEVFQLDLLSGDLR
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                                                            16.9%;
26.1%;
                              score 543.5; Db ...
pred. No. 2.5e-27;
pred. No. 2.71;
                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           August 1996
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                                           Indels 115;
                                                                                  Length
                                                                                    2610;
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                                                                                                                              838/3;
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                                                                                                                         890/2; 977/
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QY
                                                                                                                                                                                                                                                                                           C;Superfamily: rat MEGF1 protein; cadherin repeat homology; F;3798-3949/Domain: laminin G repeat homology <LGR> F;3953-3985/Domain: EGF homology <EGF1> F;3992-4023/Domain: EGF homology <EGF1>
               дЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: MEGF1
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T00252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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1803 KILEPEALKFFKIDPSMGTLTTTSELDFED-----
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                                                             65 RIVSDETIGFLLINPLTGDLLLNEKLDREELCGPTEPCVLP-FQLLLEKPFQIF-----
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---REELCGPTEPCVLPFQLLLEKPFQIFRAELWVRDINDHSPVFLDR 136
                                                                                                                                                                                        16.9%;
26.4%;
                                                                                                                                                 99;
                                                                                                                                             Score 542; DB 2; I
Pred. No. 6.8e-27;
9; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
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---TPLFQ-----FNIYVHDQGT 1847
                                                                                                                                                                                                                      Length 4351;
                                                                                                                                          Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VIDINDHAPTLIAA 482
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Db Qq

46

Matches

Conservative

82;

Mismatches

Indels

Gaps

16;

123 VRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVG-INNLRNYTISSNVYFHIN 181

LKDVNDNWPIFYPNEYHLTVREGPKPEEPLLVVSASDMDSGTFGEVSYHILSESSSFSIN 105

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: Db
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R.Du. 2.; Gattung, S.
submitted to the EMBL Data Library, May 1997
submitted to the EMBL 
                                                                                                                       A; Introns: 34/1; 114/3; 735/3; 1552/2; 1800/3; 1865/3; 1911/3; 2026/3; 2108/2; 2150/3
                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF003388; NID:g2088850; PID:g2088852; PIDN:AAB54266.1; GSPDB A;Experimental source: strain Bristol N2; clone R10F2
                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2163 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15276
                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                A; Gene: CESP:R10F2.1
                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein R10F2.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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15.1%; Score 485; DB 2; 28.9%; Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2434
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A;Cross-references: GB:D14888; NID:g457658; PIDN:BAA03605.1; PID:g457659
C;Comment: Cadherins mediate calcium-dependent intercellular adhesion and are
C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transn
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-166/Domain: propeptide #status predicted <PRO>
F;167-913/Product: R-cadherin *status predicted <PRO>
F;167-913/Product: R-cadherin *status predicted <EXT>
F;167-921/Domain: extracellular #status predicted <EXT>
F;169-274/Domain: cadherin repeat homology <CR1>
F;244-249/Region: cadherin repeat homology <CR2>
F;300-304/Domain: cadherin repeat homology <CR3>
F;301-304/Domain: cadherin repeat homology <CR3>
F;507-612/Domain: cadherin repeat homology <CR3>
F;613-721/Domain: cadherin
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C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change :
C;Date: 103-May-1994 #sequence_revision 26-May-1994 #text_change :
C;Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change :
C;Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change :
C;Date: 03-May-1994 #text_ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Cell binding specificity of mouse R-cadherin and A;Reference number: I55501; MUID:94095672; PMID:8270638 A;Accession: I55501
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A; Title: Molecular cloning of mouse pancreatic islet R-cadherin: A; Reference number: A47543; MUID:94067164; PMID:8247017
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A; Residues: 1-913 <RES>
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A; Molecule type: mRI
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VΩ
                                 C;Superfamily: cadherin; cadherin repeat homology C;Keywords: calcium binding; cell adhesion; duplicatio F;1-27/Domain: signal sequence #status predicted <SIG>
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R;Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A;Title: Diversity of the cadherin family:
A;Reference number: S24305; MUID:91283540;
A;Accession: C38992
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F;280,409,554,629,658,699/Binding site: carbohydrate (Asn) (covalent) #status predict
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C; Species: Homo sapiens (man)
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                                                                                        A;Cross-references: GDB:622850
A;Map position: 16q24.1-16qter
                                                                                                                             A; Gene: GDB:CDH4
                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-916 <SUZ>
                                                                                                                                                                                                                       A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                 C38992
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F;167-913/Product:
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Pred. No. 5.1e-22;
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                                                    duplication;
                                                                                                                                                                    PIDN: AAA35627.1;
                   <PRO>
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A; Introns: 39/1; 74/3; 122/3; 209/2; 287/3; 333/2; 489/1; 611/2; 714/1; 939/3; C; Keywords: cytoskeleton; transmembrane protein

1002/2

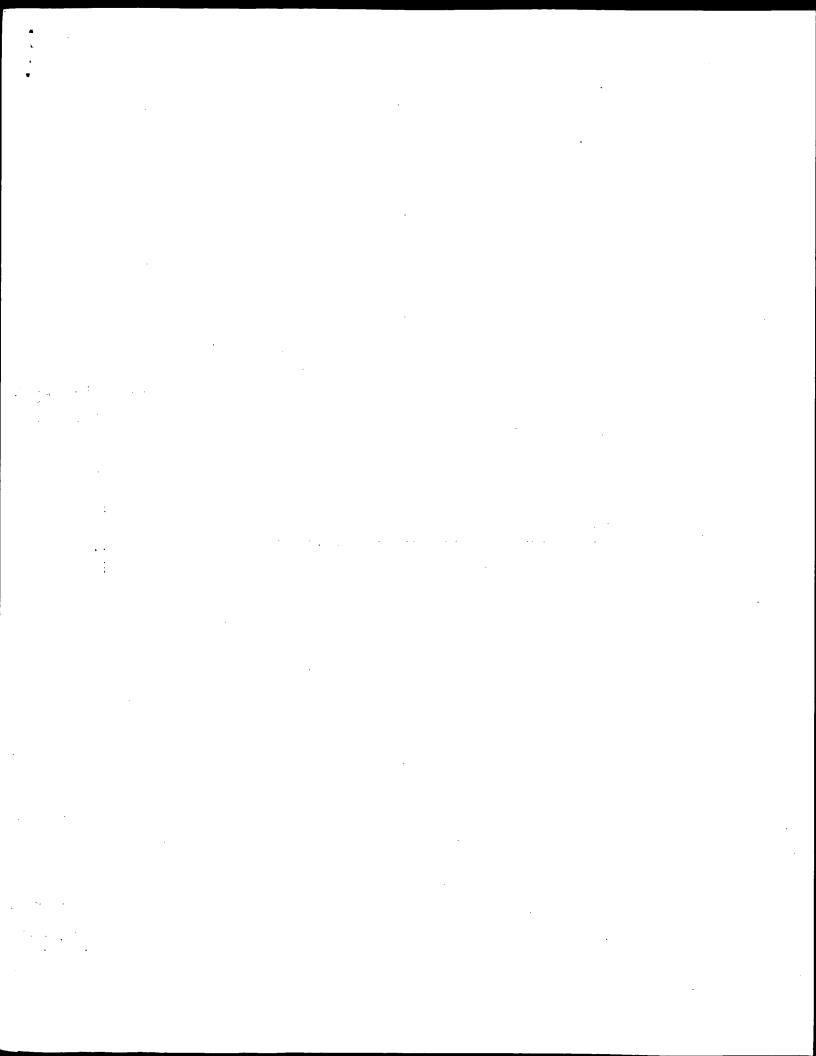
C; Genetics:

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3343 <DUZ>
                                                                                                                                  submitted to the EMBL Data
                                                                                                                                                                                 C; Acc
R; Du,
                                                                                                                                                                                          ZK112.7 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S44887
                                                                                                           A; Description: Sequence
A; Reference number: S446
A;Cross-references: EMBL:L14324; NID:g289740; PID:g289742
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F;169-274/Domain: cadherin repeat homology <CRI>F:244-249/Region: cadherin binding #status predicted
F;277-389/Domain: cadherin repeat homology <CR2>
F;300-304/Domain: calcium binding #status predicted <CAB>
F;392-504/Domain: cadherin repeat homology <CR3>
F;507-612/Domain: cadherin repeat homology <CR3>
F;517-612/Domain: cadherin repeat homology <CR3>
F;517-612/Domain: cadherin repeat homology <CR3>
F;613-721/Domain: cadherin repeat homology <CR4>
F;613-721/Domain: cadherin repeat homology <CR4>
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F;754-913/Domain: intracellular #status predicted <INT>
F;870-885/Kegion: scrine-rich
F;283,412,557,632,661,702/Binding site: carbohydrate (Asn) (covalent) #status predicted
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the C. elegans cosmid ZK112.
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 21-Jan-2000
C;Accession: G02678
R;Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.
A;Residues: 1-790 <SHI>
A;Cross-references: EMBL:U59325; NID:g1389852; PIDN:AAB02933.1; C;Superfamily: cadherin; cadherin repeat homology F;162-268/Domain: cadherin repeat homology <CDH>
                                                                                      A; Molecule type: mRNA
                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                              A; Reference number: H01584
A; Accession: G02678
                                                                                                                                                                  submitted to the EMBL Data Library, May
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Similarity 26.5%;
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Pred. No. 1.8e-20;
94; Mismatches 249;
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Search completed: May 16, 2003, 10:47:42 Job time: 30 secs



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## ALIGNMENTS

0925L6; PRELIMINARY; PRT; 723 AA.
0925L6, 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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RESULT 1
Q9251
ID 20025
AC Q9255
AC Q9255
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DF 01-D
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DF 01-J
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PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein.
NON_TER 723 723
SEQUENCE 723 AA; 79555 MW; 678543AB3647DE
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MEDLINE=21223055; PubMed=11322959;
Wanhalst K., Kools P., Vanden Eynde E., van Roy F.;
"The human and murine protocadherin-beta_one-exon_gene_families show"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:2136750; Pcdhb15.
InterPro; IPR002126; Cadherin.
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                                       1 MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS
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78.1%;
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Pred. No. 8.5e-167;
7; Mismatches 80;
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Wu Q., Maniatis T.;
"Large exons encoding multiple ectodomains are a feature of protocadherin genes.";
                                                                                                                                                                         Wu Q., Maniatis T.;
"A striking organization of like cell adhesion genes.";
Cell 97:779-790(1999).
          SEQUENCE FROM
                                        Proc.
                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                              MEDLINE=99308636; PubMed=10380929;
                                                                                                                              FISSUE=BRAIN;
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
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                                       protocadherin genes. . Acad. Sci. U.S.A. 9
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                                   97:3124-3129(2000).
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-1 SIMILARITY: CONTAINS 6 CADHI EMEL; AV013776; AAK26065.1; -.
MCD: MGI:2136750; pcdhb15.
InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycopro
SEQUENCE 786 AA; 86292 MW; OEA6C0498
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   l (TrEMBLrel. 19,
l (TrEMBLrel. 19,
2 (TrEMBLrel. 21,
                                                                                                                                        PRELIMINARY;
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7; Mismatches
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Pred. No. 9
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0EA6C04986F6FA90 CRC64;
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, Myers R.M., Ma
of mouse and hum
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"A striking organization like cell adhesion genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycoprotein.
SEQUENCE 799 AA; 87800 MM; 99C7A595F1673147 C
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Mammalia; Eutheria;
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InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20202599; PubMed=10716726;
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EMBL; AY013782; AAK26071.1;
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97:779-790(1999).
                        RIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNITITVTDLGT
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2256; DB 11;
Pred. No. 5.3e-148;
1; Mismatches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; Glycoprotein.
99C7A595F1673147 CRC64;
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PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein.
SEQUENCE 800 AA; 87537 MW; 7DF4B52E0B78A263 CR
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
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MEDLINE=2123055; PubMed=11322959;
Vanhalst K., Kools P., Vanden Eynde E., van Roy F.;
"The human and murine protocadherin-beta one-exon g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
PROSITE; PS50268; CADHERIN_2; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR002126; Cadherin.
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                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 5 CAD:
L; AF326313; AAK53238.1; -.
                 {\tt REARVYSDDNKKHLLLNLLTGDMLLNERLDREELCGSTQPCVLPFQVVLENPLQFYRAEL}
                                  EGEGLSSCRKRQVLVFFVFLGLSQASAESLRYSVAEETEIGSFVANLAKDLGLGVAELSS
                                                                                                        EARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                        evolutionary conservation, despite the
                                                                                                                                                                                                                                                                                                                                                                                                           Lett. 495:120-125(2001)
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                                                                                                                                                                         Similarity
                                                                                                                                                                                                                          844 AA;
                                                                                                                                                          Conservative
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                                                                                                                                                                      70.18;
                                                                                                                                                                                                                          93034 MW;
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                                                                                                                                                                         Score 2250;
Pred. No. 1.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                     303E780FF2E9EF7C CRC64;
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                                                                                                                                                      Mismatches
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gene clusters.";
                                                                   MEDLINE=21154914; PubMed=11230163; Wu Q., Zhang T., Cheng J.-F., Kim Dickson M., Noonan J.P., Zhang M.Q
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Wu Q., Maniatis T.;
"A striking organization of like cell adhesion genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Wammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                feature of protocadherin genes.
Proc. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                   "Large exons encoding multiple ectodomains are a feature of protocadherin genes.";
                                                                                                                                                                                                                        Wu Q., Maniatis T
                                                                                                                                                                                                                                           MEDLINE=20202599;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=99308636;
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                                                        'Comparative dna sequence analysis
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   SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                              cell adhesion genes.
97:779-790(1999).
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                                                                                                                                                                                                                                                                                                                                                                         PubMed=10380929;
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                                                                     , Grimwood J.,
Myers R.M., Ma
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                                                    protocadherin
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PIM; PF00028; cadherin; 5.
PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein.
SEQUENCE 776 AA; 84983 MW; 03F420D3098D6032 CRC64;
                                                                                                                01-DEC-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Protocadherin beta 2.
                                                                                                                                                       Q91Y00;
01-DEC-2001
                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                 PCDHB2
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                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                      Q91Y00
    TISSUE=BRAIN;
                 SEQUENCE FROM N.A.
                                           NCBI_TaxID=10090
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Rodentia;
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19,
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Last annotation updat
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                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Genome Res. 11:389-404(2001).
Genome Res. 11:389-404(2001).
Fig. SIMILARITY: CONTAINS 5 CADHE
EMBL; AV013781; AAKZ6070.1; -.
MGD; MGI:2136735; Pcdhb2.
InterPro; IPR002126; Cadherin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Large exons encoding multiple feature of protocadherin genes.
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Acad. Sci. U.S.A. 97:3124-3129(2000).
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Myers R.M., M
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycopro
SEQUENCE 784 AA; 85569 MW; 4712EAEBB
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"A striking organization of like cell adhesion genes.";
Cell 97:779-790(1999).
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Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz
Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T
"Comparative dna sequence analysis of mouse and human proto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes."; proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
               181
                                                              121
                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99308636; PubMed=10380929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protocadherin beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20202599;
                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 6 CADHERIN DOMAINS L; AY013785; AAK26074.1; - GGI:2136737; Pcdhb3.
  NVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVP
                                                                             LWVRDINDHSPVFLDREITLNILESTTPGATFILESAHDSDVGINNLRNYTISSNVYFHI
                                                  LEVIDVNDHAPEFFENAMQLKVLENSVPGTVIPLGNAVDLDVGRNGLQNYTVSPTSHFHV
                                                                                                                                                                          ARGCRIVSDETIGELLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAE 120
                                                                                                                                                                                                                                           MEAREESFLKQRQVLLLFVFLGGSLAGSMSRRYSVAEEKEKGFVIANLATDLGLSIEELA
                                                                                                                                                                                                                                                                       MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERGTFLANLAIDLGLGVEELS
                                                                                                                                               ERRAQAISKGNIQYFQLSHQTGDLLLVEKLDREDLCGSTEPCVLHFQILLHDPLQFITNE
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
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(TrEMBLrel. 19,
(TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell adhesion; Glycoprotein.
A; 85569 MW; 4712EAEB00CC2D49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10716726;
                                                                                                                                                                                                                                                                                                                                                                      67.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a large family of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                 Score 2164; DB 11;
Pred. No. 1.3e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784
                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                          Length
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; Murinae; Mus
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RESULT

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                    EMBL;
                                                                                            gene clusters.";
                                                                                                                Wu Q., Zhang T., Cheng J.-F., Kim Y.,
Dickson M., Noonan J.P., Zhang M.Q., N
"Comparative dna sequence analysis of
                    -!- SIMILARITY: CONTAINS 5 CADHERIN EMBL; AY013784; AAK26073.1; -.
                                                                      Genome Res. 11:389-404(2001).
                                                                                                                                                                                                                                                                              feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                               "Large exons encoding multiple ectodomains are a feature of protocadherin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=BRAIN;
MEDLINE=99308636; PubMed=10380929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                  TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                               Wu Q.,
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20202599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu Q., Maniatis T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protocadherin beta
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                                                                                                                                                                                       MEDLINE=21154914; PubMed=11230163;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
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ke cell adhesion genes
  MGI:2136760;
                                                                                                                                                                                                                                                                                                                                                                                                                                             97:779-790(1999).
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                                                                                                                                                                                                                                                                                                                                                               Maniatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10716726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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19,
21,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627
                                             DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family of human
                                                                                                                                       Myers R.M., M
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                                                                                                                                            Maniatis
                                                                                                                                                           Schmutz J.,
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                                                                                                                protocadherin
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RESULT Q925M6 ID Q95 MC Q9 AC Q9 DT 011 DT 012 Pr COC MC C
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Pfam; pr00028; cadherin_1; UNKNOWN_5.

PROSITE; PS00232; CADHERIN_2; 5.

PROSITE; PS50268; CADHERIN_2; 5.

Calcium-binding; Cell adhesion; Glycoprotein.

Calcium-binding; Cell adhesion; B00FB1657EA6E24A CRC64;
                                                                                                                                                                                                                                                                                                                                                               Q925M6 PRELIMINARY;
Q925M6;
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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                                      STRAIN-BALB/C;
MEDLINE-21223055;
                                                                                                 SEQUENCE FROM N.A.
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Pfam; PF00028; cadherin; 5.

PROSITE; PS00232; CADHERIN_1; UNKNOWN_5.

PROSITE; PS50268; CADHERIN_2; 6.

Calcium-binding; Cell adhesion; Glycoprotein.

Calcium-binding; Cell adhesion; Glycoprotein.
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"The human and murine protocadherin-beta
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77; Mismatches 132;
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PROSITE: PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycopro
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PROSITE;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Pfam; PF00028; cadherin; 5.
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"The human and murine protocadherin-beta one-exon gene
high evolutionary conservation, despite the difference
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Q91Y02;
Q1-DEC-2001;
Q1-DEC-2001;
Q1-JUN-2002;
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Calcium-binding; Cell adhesion; Calcium-binding; A; 86959 MW; A;
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InterPro; IPR002126; Cadherin.
InterPro; IPR003580; Protachykinin
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-!- SIMILARITY: CONTAINS 6 CADHERIN
EMBL; AY013779; AAK26068.1; -.
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Wu Q., Zhang T., Chang J.-F., Kim Y., Grimwood J.,
Dickson M., Noonan J.P., Zhang M.O., Myers R.M., Ma
"Comparative dna sequence analysis of mouse and hun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes."; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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"A striking organization like cell adhesion genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00203;
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Mammalia; Eutheria;
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""'raryota; Metazoa; Chordata;

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Wu Q., Maniatis T.;
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InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
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Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
     -:- SIMILARITY: CONTAINS 6 (EMBL; AF326311; AAK53236.1; MGD; MGI:2136756; Pcdhb18.
                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21223055; PubMed=11322959;
Vanhalst K., Kools P., Vanden Eynd
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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PROSITE; PS50266; CADHERIN_2; 6.
Calctum-binding; Cell adhesion; Glycopro
SEQUENCE 792 AA; 86897 MW; F7CA32621
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FROM N.A.
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IPR003580; Protachykinin.
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Pred. No. 8.1e-140;
                                                                  Craniata; Ver
Sciurognathi;
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                                                                                   Vertebrata; Euteleostomi;
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Best Local
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MEDLINE-21154914; PubMed=11230163;

MEDLINE-21154914; PubMed=11230163;

Mu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz

Mu Q., Zhang T., Chang M.Q., Myers R.M., Maniatis

Dickson M., Noonan J.P., Zhang M.Q., Myers and human prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.

EMBL; BC017149; AAH17149.1; -.

MCD; WGI:2136754, PGdhb17.

Interpro; IPR002126; Cadherin.

Pfam; PF00028; cadherin: 5.

PROSITE: PS00232; CADHERIN.1; UNKNOWN_4.

PROSITE: PS00232; CADHERIN.2; 6.

Calcium-binding; Cell adhesion; Glycoprotein.

Calcium-binding; Cell adhesion; Glycoprotein.
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"Large exons encoding multiple ectodomains feature of protocadherin genes.";
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"A striking organization of
like cell adhesion genes.";
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Proc. Natl. Acad. Sci. U.S.A. 9
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      ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS
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                                                                                      LHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENS
                                                                                                                                          \tt KFQQPTYRVQIPENSPTGSLVLTVSANDLDSGDYGKVLYALSQPSEDISKTLEVNPVTGE
                                                                                                                                                                   EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN
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Pred. No. 1
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Search completed: May 16, 2003, 10:48:22 Job time : 41 secs

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US-10-175-738-478

US-10-175-738-478

US-10-176-482-478

US-10-176-913-478

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; Sequence 125, Application US/10050704
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/11
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/11
PRIOR FILING DATE: 1998-12-22
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Publication No. US20020192751A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26
CURRENT FILING DATE: 2001-12-86
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PRIOR FILING DATE: 1998-12-23
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Stewart, Timothy A.
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OR FILING DATE: 1999-06-08
OR APPLICATION NUMBER: 60/144791
OR FILING DATE: 1999-07-20
OR APPLICATION NUMBER: 60/146970
OR APPLICATION NUMBER: 60/146970
OR FILING DATE: 1999-08-03
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OR APPLICATION NUMBER: 60/131291

OR APPLICATION NUMBER: 60/132371

OR APPLICATION NUMBER: 60/132371

OR FILING DATE: 1999-05-04

OR APPLICATION NUMBER: 60/132379

OR FILING DATE: 1999-05-04

OR APPLICATION NUMBER: 60/132383

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APPLICATION N
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APPLICATION NUMBER: 09/869599
FILING DATE: 2001-06-29
APPLICATION NUMBER: 09/908,827
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APPLICATION NUMBER: 09/874503
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FILING DATE: 2001-05-10
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APPLICATION NUMBER: 09/644848
FILING DATE: 2000-08-22
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FILING DATE: 1999-04-21
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FILING DATE: 1999-04-27
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                              NUMBER: PCT
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RESULT 3
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-041-52
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Best Local Similarity 70.4%;
Matches 435; Conservative
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OR APPLICATION NUMBER: PCT/USO1/06520
OR FILING DATE: 2001-02-28
OR FILING DATE: 2001-06-01
OR FILING DATE: 2001-06-01
OR APPLICATION NUMBER: PCT/USO1/19692
OR APPLICATION NUMBER: PCT/USO1/19692
OR FILING DATE: 2001-06-20
OR FILING DATE: 2001-06-29
OR FILING DATE: 2001-06-29
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                                                                                             TEPGLFGVWAHNGEVRTA 627
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                                                                                                                                                                        LVADANDNAPFYLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA 609
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Pred. No. 1.2e-157;
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GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C4
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
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DR APPLICATION NUMBER: 60/132371

DR FILING DATE: 1999-05-04

DR APPLICATION NUMBER: 60/132379

DR FILING DATE: 1999-05-04

DR APPLICATION NUMBER: 60/132383

DR FILING DATE: 1999-05-04

DR APPLICATION NUMBER: 60/132383

DR FILING DATE: 1999-05-04

DR APPLICATION NUMBER: 60/135750

DR FILING DATE: 1999-05-25
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FILING DATE: 1999-03-23
APPLICATION NUMBER: 60/125826
FILING DATE: 1999-03-24
APPLICATION NUMBER: 60/127035
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FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/114140
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FILING DATE: 1998-12-23
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FILING DATE: 1999-03-23
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FILING DATE: 1999-06-08
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APPLICATION NUMBER: 60/
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FILING DATE: 1999-04-21
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Goddard, Audrey
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SEQ ID NO 52
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nes 435; Conserv
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APPLICATION NUMBER: PCT/US00/34956
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VYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVPEFVESLYKV 249
                                  APVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM 189
                                                                       SPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHINVHDNGEGN 189
                                                                                                             DNKQYLLLDSHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDINDH 129
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APPLICATION NUMBER: PCT/US00/15264
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APPLICATION NUMBER: 09/747259
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APPLICATION NUMBER: 09/644848
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Pred. No. 1.2e-157;
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
LENGTH: 800
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ACIDS ENCODING FILE REFERENCE: P3430R1C42
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                 RQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAARGTRVVSD
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                                                                     Matches 435;
                                                                                                                                                                                                    FILE REFERENCE: 93430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
SEQ ID NO 478
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Sequence 478, Application US/10176758
                                                                                                     Query Match
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                          70.1%; 5-
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                                                                                 Score 2249; DB 9; Pred. No. 1.2e-157;
                                                                   Mismatches
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                                                     US-10-175-737-478
                                                                                   CURRENT FILING DATE: 2002-06
Prior Application removed - S:
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
LENGTH: 800
TYPE: PRT
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                                                                                                                                                                                    APPLICANT: Zhang,Zemin APPLICANT: Zhang,Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C50
CURRENT APPLICATION NUMBER: US/10/175,737
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Gurney, Austin L.
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 Score 2249;
Pred. No. 1
19; DB 9;
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Best Local Similarity

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         Prior Application removed -
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
                                                                                                                                                                                                                                                     Sequence 478, Application US/10173706 Publication No. US20030022293A1 GENERAL INFORMATION:
                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: p3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
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Gurney, Austin L.
                                                                                                                         Wood, William I.
                                                                                                                                        Watanabe, Colin K.
                                                                                                                                                                 Pan, James
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GENERAL INFORMATION: APPLICANT: Baker, Ke
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                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
CURRENT APPLICATION NUMBER: US/10/175,738 CURRENT FILING DATE: 2002-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 QVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGNLHLKAELNY
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Godowski, Paul
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                                                                                                                                                            Watanabe, Colin K.
                                                                                                                                                                                      Smith, Victoria
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Pred. No. 1.2e-157;
'0; Mismatches 113;
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-478
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
            APPLICANT:
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                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                              Sequence 478, Application US/10175752 Publication No. US20030022295A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                              QVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGNLHLKAELNY 309
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                                                                                      Desnoyers, Luc
Goddard, Audrey
Smith, Victoria Watanabe, Colin K. Wood, William I.
                                                        Godowski, Paul J. Gurney, Austin L.
                                             Pan, James
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RESULT 10 US-10-176-482-478

Sequence 478, Application US/10176482 Publication No. US20030022296A1 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul

Desnoyers, Luc Goddard, Audrey Godowski, Paul J Gurney, Austin

APPLICANT:

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TYPE: PRT
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Matches 435
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LENGTH: 800
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CURRENT FILING DATE: 2002-06-19
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            TEPGLFGVWAHNGEVRTA 627
                                                         LVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKA
                                                                         LVADANDNAPFYLYPLQNGSAPCTELVPRAAEAGYLVAKVVAVDGDSGQNAWLSYQLLKA
                                                                                                                    LLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPALSSQALVRV
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
LENGTH: 800
TYPE: PRT
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Smith, Victoria
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70.48;
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Pred. No. 1.
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1.2e-157;
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US-10-176-757-478
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LENGTH: 800
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CURRENT FILING DATE: 2002-06-20
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Similarity 70.4%; Pred. No. 1
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Sequence 478, Application US/10176757 Publication No. US20030022297A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.

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CURRENT APPLICATION NUMBER: US/10/176,913

CURRENT FILING DATE: 2002-06-20
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CURRENT FILING DATE: 2002-06-25
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 478
LENGTH: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME EILE REFERENCE: 94430R1C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
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Wood, William I.
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Gurney, Austin L.
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PRIOR APPLICATION NUMBER: 60/112514
PRIOR APPLICATION NUMBER: 60/113510
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
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CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/085579
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FILING DATE: 1999-04-05
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FILING DATE: 1999-01-22
APPLICATION
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                                                  FILING DATE: 1999-04-27
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Gurney, Austin L.
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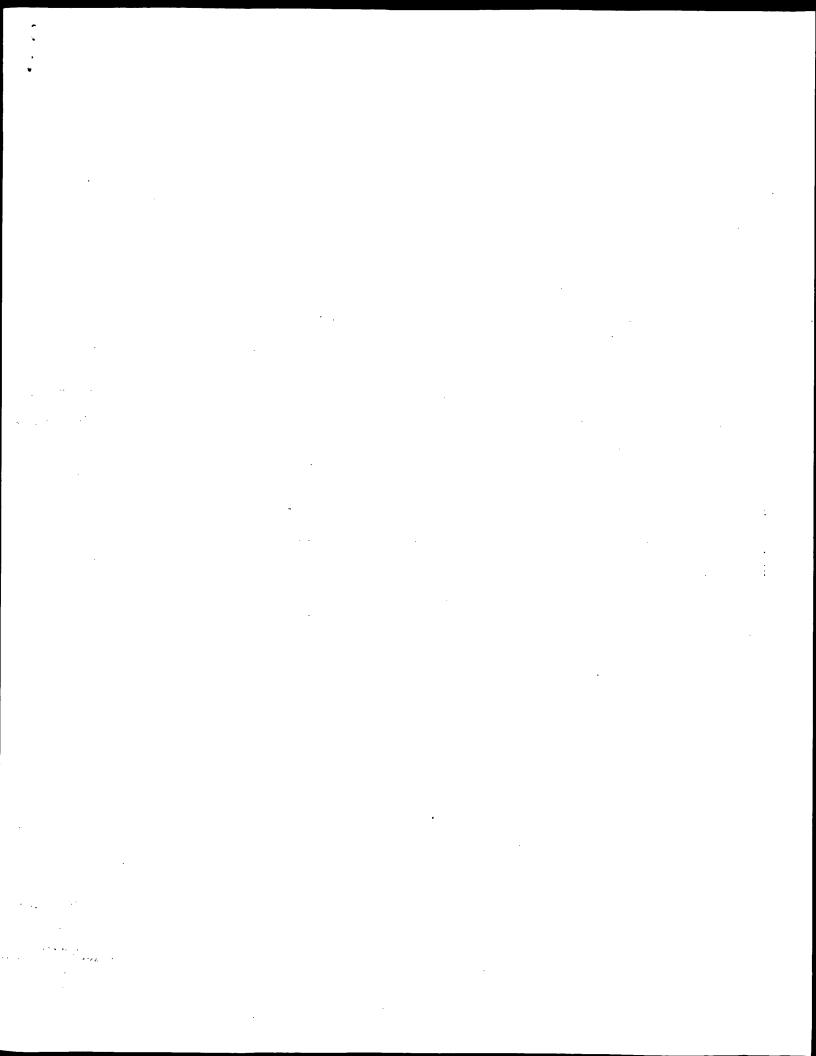
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; NUMBER OF SEQ ID NOS: 8; SEO ID NO 52; LENGTH: 800; TYPE: PRT; ORGANISM: Homo Sapien US-09-931-836-52
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APPLICATION NUMBER: 09/747259
APPLICATION 2000-12-20
APPLICATION NUMBER: 09/747259
                                                                                                                             APPLICATION NUMBER: PCT FILING DATE: 2001-07-09
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FILING DATE: 2000-08-23
APPLICATION NUMBER: PCT/US00/23328
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APPLICATION NUMBER: 60/146970
FILING DATE: 1999-08-03
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FILING DATE: 1999-05-04
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FILING DATE: 2000-12-20
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Search completed: May 16, Job time : 27 secs 2003, 10:48:51



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                    SwissProt_40:*
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                    CDB1_HUMAN
CDA5_HUMAN
CDA5_HUMAN
CHC2_HUMAN
CDA0_HUMAN
CDA1_HUMAN
CDA7_HUMAN
CDA7_HUMAN
CDA6_HUMAN

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0634fl rattuu
09y5f3 homo:
09y5f3 homo:
09y5f4 homo:
09y5f4 homo:
09y5f4 homo:
09y5f3 homo:
09y5f3 homo:
09y5f3 homo:
09y5f3 homo:
09un72 homo:
09un73 homo:
09un73 homo:
09un73 homo:
09un73 homo:
09un75 homo:
09y5f6 homo:
09un75 homo:
09y5f6 homo:
09y5f7 homo:
09y5f8 homo:
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Q9y5e7 homo
Q9y5e9 homo
Q9y5e8 homo
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09un66
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Q9y5e5
Q9y5f1
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Q9un67
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8 rattus norv
3 homo sapien
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9 homo sapien
1 homo sapien
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CDB7_HUMAN
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Result No.

4.5	44	43	42	41	40	39	38	37	36	35	34
584	. 585	589	590	595.5	597	598.5	599	603	703	807	880.5
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CLR1_MOUSE	CADN_HUMAN	STAN_DROME .	CLR1_HUMAN	CLR2_HUMAN	FAT_DROME	CLR3_HUMAN	CLR3_MOUSE	CLR3_RAT	PC16_HUMAN	PCD7_HUMAN	PC12_HUMAN
035161 mus											
mus musculu	o sapien	sophila	o sapien	o sapien	sophila	o sapien	musculu	tus norv	no sapien	no sapien	o sapien

## ALIGNMENTS

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TENTIAL. OTOCADHERIN BETA 7.	卢버	PS00232; CADHERIN_1;	PRINTS; PRO0205; CADHERIN.	Pfam; PF00028; cadherin; 5.	67;	6	; HGNC:8	HSSP: P15116: 1NCJ.	EMBL; AF152500; AAD43761.1;		an email to license@isb-sib.ch).	entities requires a license agreement (see http://www.ish.esh.ch/announce/entities requires a license agreement (see http://www.ish.esh.ch/announce/	non-profit institutions as long as its content is in no	European Bioinformatics Institute. There are no res	between the Swiss Institute of Bioinformatics and the EMBL outstation .	entry is copyright.	CHRIDALIA COMINING CADARAIN DOMAINS.	-:- SUBCELLULAK LUCATION: Type I membrane protein (By similarity).	-!- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.	FEBS Lett. 495:120-125(2001).	number. ";	The numen and murine protocadnerin-beta one-exon gene families show high evolutionary conservation, despite the difference in gene	LIST K., Kools P., Vanden Eynde E., van Roy F.;	3055; PubMed=11322959;	SEQUENCE FROM N.A.	[2]	Cell 97:779-790(1999).	"A Striking organization of a large family of human neural cadherin-		MEDLINE=99308636; PubMed=10380929;	SEQUENCE FROM N.A.	[1]	la; Primates;		Homo sapiens (Human).	**************************************	in bet	Last	2001 (Rel. 40, Creat		CDB7_HUMAN STANDARD; PRT: 793 AA

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RESULT
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                                                                                                                                   GTNAQVIYSLLPSQDPHLPLASLVSINADNGHLFALRSLDYEALQAFEFRVGATDRGSPA
                                                                                                                                                                                   GANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSPA
                                                                                                                                                                                                                      ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS
                                                                                                                                                                                                                                              PETVVAVFRIRDRDSGNNGKTVCSIQDDVPFILKPSVENFYTLVTEKPLDRERNTEYNIT
                                                                                                                                                                                                                                                        PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
                                                                                                                                                                                                                                                                                   LHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENS
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                                                                                                                                                                                                                                                                                                                                                                                              LWVRDINDHAPVFLDREISLKILESTTPGAAFLLESAQDSDVGTNSLSNYTISPNAYFHI
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(Rel. 4)
(Rel. 4)
(Rel. 4)
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       precursor (PCDH-beta2)
               Last sequence update)
Last annotation update
                                   Created)
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
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CADHERIN 3.
CADHERIN 4.
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E5677098653CC755
                                                     PRT;
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No. 3.9e-176;
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GLCNAC...
GGLCNAC...
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                update)
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) (POTENTIAL).
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CARBOHYD
SEQUENCE
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DOMAIN
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FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00232; CADHERIN_1; 5. PROSITE; PS50268; CADHERIN_2; 6. Calcium-binding; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                            Transmembrane;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu Q., Maniatis T.;
"A striking organization of like cell adhesion genes.";
Cell 97:779-790(1999).
                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:8687; PCDHB2.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 604967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21223055; PubMed=11322959; Vanhalst K., Kools P., Vanden Eynde E., Vanden human and murine protocadherin-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99308636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 high evolutionary
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                                                          FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN. SUBCELLULAR LOCATION: Type I membrane protein (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
GKKMHLQFDRQTGDLLLNEKLDREELCGPTEPCVLPFQVLLENPLQFFQAELRIRDVNDH
          ETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLFFQLLLEKPFQIFRAELWVRDINDH 129
                                             KQRQVLIFFVLLGIAQASCQPRHYSVABETESGSFVANLLKDLGLEIGELAVRGARVVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF152495;
AF217756;
                                                                                                                                                                                                                                                                                                                                                                                     SM00112; CA; 6.
                                                                                                         Similarity
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                                                                                             Conservative
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Chordata;
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                                                                                                                                            569 I
87253 MW;
                                                                                                       72.4%;
73.0%;
                                                                                                                                                                                                                                                                                                                                         family.
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CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
N-LINKED (GL
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N-LINKED (GL)
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CYTOPLASMIC
CADHERIN 1.
                                                                                            Score 2323; DB 1;
Pred. No. 1.7e-147;
5; Mismatches 102;
                                                                                                                                                                                                                                                                                                    EXTRACELLULAR
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                                                                                                                                            LINKED (GLCNAC.
B2602E865378CB27
                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal; Repeat;
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D (GLCNAC. .
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ta one-exon gene
e the difference
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(POTENTIAL).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Profocadherin beta 14 precursor (PCDH-beta14).
                                                                                                        SEQUENCE FROM N.A.
MEDIINE-21223055; PubMed-11322959;
Vanhalst K., Kools P., Vanden Eynde E., v
"The human and murine protocadherin-beta
high evolutionary conservation, despite t
                                                                                       FEBS
                                                                                                                                                                        Cell
[2]
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalia; Eutheria;
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                                                                                                                                                                                  Q., Maniatis T.;
striking organization of
ke cell adhesion genes.";
11 97:779-790(1999).
                                            S Lett. 495:120-125(2001).

FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION SUBCELLULAR LOCATION: Type I membrane protein (By SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEPGLFGVWAHNGEVRTA 627
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PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycoprotein; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF217744;
HSSP; P15116; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF152493; AAD43754.1;
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                                                                                                                                                                      LHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPENS
                                                                                           PETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
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ITYTOLGTPRLKTEYNITYLLSDVNDNAPTETQTSYTLEVRENNSPALHIGSVSATDRDS
                     ITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRDS
                                                                          SETLVALFSILDQDSGDNGRMICSIQDNLPFFLKPTFKNFFTLVSEKALDRESQAEYNIT
                                                                                                                                                    VNLRSPLDFEVIQSYTINIQATDGGGLSGKCTLLVKVMDINDNPPEVTISSITKRIPENA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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71.3%;
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N-LINKED (GLCNAC. . .) (POT N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. .) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2306; UB 1,
Pred. No. 2.3e-146;
8; Mismatches 102;
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CADHERIN
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DOMAIN
                                                                                                                     PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The
                                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCDHB1
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Q9Y5E8;
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                                   TRANSMEM
                                                    DOMAIN
                                                                        CHAIN
                                                                                       SIGNAL
                                                                                                      Transmembrane; Multigene
                                                                                                                                                                           PRINTS; PRO0205; CAI
SMART; SM00112; CA;
                                                                                                                                                                                                                 Pfam; PF00028; cadherin;
                                                                                                                                                                                                                                                                                        Genew; HGNC:8686;
                                                                                                                                                                                                                                                                                                       EMBL; AF152494; AAD43755.1; -. EMBL; AF217742; AAK51610.1; -.
                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vanhalst K., Kools P., Vanden Eynde E., van Roy F.; "The human and murine protocadherin-beta one-exon g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=21223055; PubMed=11322959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu Q., Maniatis T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99308636; PubMed=10380929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 15 precursor (PCDH-beta15)
                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION SUBCELLULAR LOCATION: Type I membrane protein (By si SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  triking organization of a large cell adhesion genes."; 97:779-790(1999).
                                                                                                                                                                                                                                                      604967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            evolutionary conservation, despite the difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLSYQLLKATEPGLFGVWAHNGEVRTA 627
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                                                                                                                                                                                                                                  IPR002126; Cadherin.
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Primates; Catarrhini;
              POTENTIAL.
CYTOPLASMIC
                                                  PROTOCADHERIN EXTRACELLULAR
                                                                                       POTENTIAL.
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              (POTENTIAL).
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                                                    (POTENTIAL).
                                                                   BETA 15
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CARBOHYD
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                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                          16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                  Q9Y5E6;
                                                                                                                                                                                                                   CDB3_HUMAN
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                NCBI_TaxID=9606;
[1]
                                                                                                        PCDHB3
                                                                                     Homo sapiens (Human)
                                                                                                                         Protocadherin
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
in beta 3 precursor (PCDH-beta3)
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Pred. No. 4.2e
67; Mismatches
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8DE8D3A07B0B6A56 CRC64;
                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF217755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002126; Cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 604967;
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SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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S LOTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.

FUNCTION: TYPE I membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
NVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVP
                                                                                                                                                                                                                                                      MEARVVHALQKRQVSLLCVFLGVSWAGAEPLRYFVAEETERG: FLANLAIDLGLGVEELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alst K., Kools P., Vanden Eynde E., van Roy F.;
human and murine protocadherin-beta one-exon gene
evolutionary conservation, despite the difference
                                          LRIIDVNDHSPVFFENEMHLKILESTLPGTVIPLGNAEDLDVGRNSLQNYTITPNSHFHV
                                                                       LWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHI 180
                                                                                                                               ARGAQVVSKGNKQHFQLSHQTGDLLLNEKLDREELCGPTEPCILHFQILLQNPLQFVTNE
                                                                                                                                                                     ARGCRIVSDETIGELLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLEKPFQIFRAE
                                                                                                                                                                                                                MEAGGERFLRQRQVLLLFVFLGGSLAGSESRRYSVAEEKEKGFLIANLAKDLGLRVEELA
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                                                                                                                                                                                                                                                                                                                           Similarity
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Pred. No. 2
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                                             This
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                                                                                                                                                                                                                 MEDLINE=20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
"YVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
                                                                                                       Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 16 precursor (PCDH-beta16) (Protocadherin 3x).
PCDHB16 OR PCDH3X OR KIAA1621.
                           between the
                                                                                                                                         cluster."
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             one-exon
                                                                                                                                                                       Kools
                                                                                                                                                                                                                                                                                               MEDLINE=20450683;
                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                               "The human protocadherin one-exon genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; vertebrata; butere
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NRJ7; Q9HCF1;
                                                                                                                                                      "Molecular analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                         SUBCELLULAR LOCATION: Type I membrane protein (By similarity). SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                       van Roy F.M.;
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                                                                                                                                                      the human protocadherin-3 (PCDH-Beta)
                                                                                                                                                                                                                                                                                                                                                                                       3 gene cluster,
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF217757; AAF81914.1;
EMBL; AB046841; BAB13447.1;
EMBL; AF282973; AAG10030.1;
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MIM; 604967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:14546; PCDHB16
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PEIVVAVFSVSDPDSGNNGKTISSIQEDLPFLLKPSVKNFYTLVTERALDREARAEYNIT
         PETVVAVFRIRDRDSGNNAKMYCSIQDHLPFVLKPSVENFYTLVTERALDREERTEYNIT
                                    VRLRKQVDFEMVTSYEVRIKATDGGGLSGKCTLLLQVVDVNDNPPQVTMSALTSPIPENS
                                                       LHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTYVVHVTDINDNPPELLMSSLTSPIPENS
                                                                                                              LIHEFROGRKYPELVLOKELDREEEPQLRLTLTALDGGSPPRSGTAQVRIEVVDINDNAP
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                                                                                                                                                                                       TRKARTISQGNKQHLQLKAQTGDLLINEKLDREELCGPTEPCILHFQVLMENPLEIFQAE
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                                                                          EFEQPIYKVQIPENSPLGSLVATVSARDLDGGANGKISYTLFQPSEDISKTLEVNPMTGE
                                                                                            EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN
                                                                                                                                                                                                                                                                         Similarity
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0028; cadherin; 5.
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                                                                                                                                                                                                                                                                                                 CADHERIN.
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T-> I (IN REF. 2).
QA-> RE (IN REF. 2).
G-> S (IN REF. 2).
R-> S (IN REF. 2).
Q-> H (IN REF. 2).
Q-> H (IN REF. 2).
R-> C (IN REF. 2).
R-> C (IN REF. 2).
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Pred. No. 1
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CADHERIN
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-> V (IN REF. 2).
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.pP00028; cadherin; 5.
.rINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS00232; CADHERIN_2; 6.
CAlcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
Transmembrane; Multigene family.
Transmembrane; Multigene family.
TSICKAL
1 269 PROTOCADHERIN BETA 10.
DOMAIN 27 692 EXTRACELLULAR (POTENTIAL.
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TRANSMEM 693 133 CADHERIN 1.
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59 169
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Cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as iving ... sage by and for communication modified and this statement is not removed. Usage by and for communication modified and this statement is not removed. Usage by and for communication modified and this statement is not removed. Usage by and for communication modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UN67;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99308636;
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN. SUBCELLULAR LOCATION: Type I membrane protein (By similarity). SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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Primates;
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Last annotation update)
precursor (PCDH-beta10)
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CARBOHYD
                                                     SEQUENCE FROM N.A. MEDLINE=99308636;
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Sapiens (Human).
ryota; Metazoa; Chordata; Craniata; Vertebrata;
ryota; Metazoa; Primates; Catarrhini; Hominidae
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Pred. No. 1.5e-142;
0; Mismatches 113;
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PROSITE; PS50268; CADHERIN_2; 6
Calcium-binding; Cell adhesion;
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"Human protocadherin
Submitted (NOV-2000)
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Pfam; PF00028; cadherin;
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EMBL; AF217749; AAF81913.1; -.
EMBL; AF282973; AAG10032.1; -.
HSSP; P15116; 1NCJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cell 97:779-790(1999).
                                                                                                                                                                                                                                                         SEQUENCE
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CDB4_HUMAN STANDING
CDP4_CDT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41 precursor (PCDH-beta4).
                                                                                                                                                                          number
                                                                                                                                                                                                                                                                                  MEDLINE=21223055; PubMed=11322959;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Wu Q., Maniatis T.;
"A striking organization of like cell adhesion genes.";
Cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                 Vanhalst K.,
"The human a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=99308636;
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                                                      FUNCTION: POTENTIAL CALCIUM-DEPENDENT CE
SUBCELLULAR LOCATION: Type I membrane pr
SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
              SWISS-PROT
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                                                                                                                                          495:120-125(2001)
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           entry
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PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 5.
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MIM; 604967;
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HSSP; P15116; 1N
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RESULT 10
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    TRANSMEM DOMAIN
                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long or modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FKUM N.A.
MEDLINE-21223055; PubMed-11322959;
Vanhalst K., Kools P., Vanden Eynde E., van Roy F.;
"The human and murine protocadherin-beta one-exon gene
"The human and murine protocadherin despite the difference
                                                                   PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2; Calcium-binding; Cell adhesion
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 12 precursor (PCDH-beta12)
                                               SIGNAL
                                                           Transmembrane;
                                                                                                               Pfam; PF00028; cadherin; 5
PRINTS; PR00205; CADHERIN.
                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                               number.
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                          DOMAIN
                                                                                                                                    InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 495:120-125(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A striking organization of a large like cell adhesion genes.";
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                                                                                                                                                                                                                                                                                                             FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN. SUBCELLULAR LOCATION: Type I membrane protein (By similarity SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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                                                                                                     SM00112; CA;
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; CADHERIN_2; 6.
Cell adhesion; Glycoprotein;
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            PROTOCADHERIN BETA 12.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
  CYTOPLASMIC (POTENTIAL)
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 RESULT 11
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Best Local :
                                   QYY5E4; Q9UFU9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
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                                                           LSSEALVRVLVLDANDNSPFVLYPLQNGSAPCTELVPWAAEPGYLVTKVVAVDGDSGQNA
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PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein;
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EMBL;
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN
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-i- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS
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Similarity
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6.3e-138;
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DT 16-OCT
DT 15-JUN
DE PTOTOCO.
GN PCDHB6
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16-OCT-2001
16-OCT-2001
15-JUN-2002
SEQUENCE FROM N.A.
MEDLINE-21223055; PubMed-11322959;
Wanhalst K., Kools P., Vanden Eynde E., V
"The human and murine protocadherin beta
high evolutionary conservation, despite t
                                                                                      Wu Q., Maniatis T.;
"A striking organization like cell adhesion genes. Cell 97:779-790(1999).
                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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-I- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity
-I- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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IRLRKALDFEEIQSYDVDVEATDGGGLSGKCSLVVRVLDVNDNAPELTMSFFISLIPENL
                                                    EFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSGN
                                                                                      LTRNRSEGRKFPELVLDKPLDREEQPQLRLTLIALDGGSPPRSGTSEIQIQVLDINDNVP
                                                                                                                                                       LWVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFHI 180
                                           EFAQELYEAQVPENNPLGSLVITVSARDLDAGSFGKVSYALFQVDD-
                                                                                                             NVHDNGEGNVYSELVLDKVLDREEVPELRLTLTGLDGGSPPRSGTTLIRILVLDINDNVP
                                                                                                                                   LRVRDINDHAPEFPAREMLLKISEITMPGKIFPLKMAHDLDTGSNGLQRYTISSNPHFHV
                                                                                                                                                                             {\tt SRGARVVFKGNRQHLQFDPQTHDLLLNEKLDREELCGSTEPCVLPFQVLLENPLQFFQAS}
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                                                                                                                                                                                                                                                                       430;
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                                                                                                                                                                                                                                                                                  Similarity
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87349 MW;
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68.6%;
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 4.
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CADHERIN 6.
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No. 1.4e-137;
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                                                                                                                             EMBL; AF152490; AAD43751.1; -. EMBL; AF217747; AAK51615.1; -. HSSP; P15116; 1NCJ.
                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                        FEBS Lett. 495:120-125(2001).
-!- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity
                                                                                                                                                                                                                                                                                                                                                                               Vanhalst K., Kools P., Vanden Eynde E., van Roy F.; "The human and murine protocadherin-beta one-exon gene high evolutionary conservation, despite the difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=99308636; Wu Q., Maniatis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Y5F2;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                  MIM; 606337;
                                                                                                               Genew; HGNC:8682;
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=21223055; PubMed=11322959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A striking organization like cell adhesion genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Type I membrane protein -!- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
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PROSITE; PS00232; CADHERIN\_1; PROSITE; PS50268; CADHERIN\_2;

PROSITE;

PRINTS; PR00205; CAI SMART; SM00112; CA; Pfam; PF00028; cadherin; 5 PRINTS; PR00205; CADHERIN. MIM; 604967;

InterPro; IPR002126; Cadherin

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68.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:8693; PCDHB8
MIM; 606334; -.
MIM; 604967; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu Q., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PODHB8 OR PCUMAN).
Homo sapiens (Human).
Horvota; Metazoa; Chordata;
horvia; Primates;
                                                                                                                                                                                                                                                                                            Transmembrane; SIGNAL
                                                                                                                                                                                                                                                                                                        PROSITE; PS00232; CADHERIN_1; 5.
PROSITE; PS50268; CADHERIN_2; 5.
Calclum-binding; Cell adhesion; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A striking organization of cadherin-like cell adhesion cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular analysis of the human cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu Q., Maniatis T.;
Submitted (NOV-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protocadherin beta 8 precursor (PCDH-beta8) (Protocadherin PCDHB8 OR PCDH31.
                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF152501; AAD43762.2; EMBL; AF282973; AAG10031.1;
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"A striking orga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein (By similarity). SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
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Q-> L (IN REF. 3)

Q-> L (IN REF. 3)
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                      V REF. 3).
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There are no restrictions
on as its content is in
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16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
Protocadherin beta 13 precurso
                                                                MEDLINE=99308636; PubMed-
Wu Q., Maniatis T.;
"A striking organization
like cell adhesion genes.
                                                                                                                                         PODHB13,
Homo sapiens (Human).
Homo sapiens (Human).
"Torta; Metazoa; Chordata; "
                                                                                                                                                                                                                                                                       CDBD_HUMAN
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                          SEQUENCE FROM N.A.
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              MEDLINE-21223055;
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precursor (PCDH-beta13).
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PROSITE; PS50268; CADHERIN_2; 5.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 495:120-125(2001).
i- FUNCTION: POTENTIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
i- SUBCELLULAR LOCARION: Type I membrane protein (By similarity.
i- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The human and murine protocadherin-beta one-exon gene high evolutionary conservation, despite the difference
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HSSP; P15116; 1
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            NLHLKAELNYEAIQTYTLTIQAKDGGGLSGKCTVVVHVTDINDNPPELLMSSLTSPIPEN
                                                                                                SARGCRIVSDETIGFLLLNPLTGDLLLNEKLDREELCGPTEPCVLPFQLLLLEKPFQIFRA
 EIELKKQLDFEKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPEN
                                                             PEFVESLYKVQVPENSPVGSLVVTVSARDLDTGSNGEIVYAFFYATERTLKTFRINSTSG
                                                                                                                                                                ELMVRDINDHSPVFLDREITLNILESTTPGATFLLESAHDSDVGINNLRNYTISSNVYFH
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                                                 PEFEQPFYRVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTG
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VWAHNGEVRTA 627            WAHNGEVRTA 627	ALSSEALVRVVVLDANDNSFFVLYPLQNGSAPCTELVPRAAEGGYLVKKVAAVGGUSGQN 599	480 SGTNAQVTYSLLPPQDPHLPLTSLVSINADNGHLFALRSLDYEALLGGFQFRVGASDHGSP 539	SGANAQVTYSLLPPHDPQLPLGSLVSINADNGQLFALRSLDFEALQAFEFRVGAADRGSP 539	420 TITVTDLGTPMLITQLNMTVLIADVNDNAPAFTQTSYTLFVRENNSPALHIRSVSATDRD 479	420 TITVTDLGTPRLKTQHNLTVTVSDVNDNAPTFSQTTYTLRVRENNSPALHIGSVSATDRD 4	361 APETVVALESVSDLDSGENGKISCSIQEDLPFLLK-SAENFYTLLTERPLDRESRAEYNI	360 SPETVVAVFRIRDRDSGNNAKMVCSIQDHLPFVLKPSVENFYTLVTERALDREERTEVNI 4
	565	539	339	179	479	419	419

Search completed: May 16, 2003, 10:46:24 Job time: 19 secs